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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-854-549A-1

US-08-854-050-224

US-09-430-323-224

US-09-572-423B-3

US-09-572-423B-3

US-09-675-321-1

US-09-675-321-1

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US-09-675-919-1

US-09-732-2486-1

US-09-721-456-1

US-09-721-456-1
       US-08-864-050-173

US-09-4210-323-173

US-09-402-181B-292

US-09-721-456-292

US-08-974-549A-4

US-08-912-951-4

US-08-912-951-4

US-09-402-181B-4
                                                                                                            US-08-974-549A-343
US-09-402-181B-343
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                            FILING DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: 18-APR-1997
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06
FILING DATE: 06-MAY-1997
CLASSIFICATION:
                                                       ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/846,017
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               FILING DATE: 01-OCT-1996 CLASSIFICATION:
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            TELEPHONE:
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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(415) 576-0300
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FR: 015389-002930US
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LOCATION: 56..3454
OTHER INFORMATION: /
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Best Local Similarity 100.
Matches 4015; Conservative
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LENCTH: 4015 base pairs
TYPE: nucleic acid.
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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                                        /product= "hTRT"
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component"
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RESULT 2 US-08-974-549A-1 ; Sequence 1, Application US/08974549A ; Patent No. 6166178	3961 GAGGTGCTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015	Qy 3841 AGGIGGAGCCCTGAGAGGACCCTGGGAGCTCTGGGAGTTTGGAGTGACCAAAGGTGTG 3900	3721 GGGCCAGCTITICCTCACCAGGAGCCCGGCTTCCACCCACATAGGAATAGTCCATCCGGCGTTCCACCCCACCACCACCCCACCACCCCACCACCCGCGCCTTCGCCTTTGCCTTTCCACCCCCACCACCCCCACCACCCCCCCC	3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	Db 3541 CACACCCAGGCCGCACGCCTGGGAAGTCTGAGGCCTGAGGTGTTTTGGCCGAGGCCTG 3600 Qy 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCAGGC	Qy 3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG	3361 GTGAGTCGGAAGCTCCCGGGGACGCCTACTGGACTGCCCTGGAGGCCGAGCCGAGCCGGCGAGCCCGGCGAGCCCGGCGAGCCCGGCGAGCCCGGAGCCGAGCCGGGCGAGCCGAGCCGAGCCGGAGCGAGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCAGGCCGGCCGAGACCGGCCGAGACCGGCCGGACGGCCGAGGCCGAGGCCGAGGCCGAGGCCGGCCGGCCGGCCGAGAGGCCAGGCCGGCCGGACGGCCGGCCGGCCGAGGCCGGCCGGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGAGGCCGGGCCGAGGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGCCGGACGGCCGGCCGGCCGGCCGGGCCGGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGACGGCCGGCCGGCCGGCCGGGCCGGGCCGGACGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGGCCGGGCCGGACGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGGCCGGCGGGCGGGCGGCGGCGGCGGGG	Qy 3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360	ωωω	3121 TCAGCA 3121 TCAGCA 3181 CTGCTA	Qy 3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

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FILING DATE: 01-OCT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

APPLICATION UNUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: APPLE, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELEPOMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION UNMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION UNMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION UNMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION UNMBER: US 08/911,312

APPLICATION UNMBER: US 08/911,312

FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/176
APPLICATION NUMBER: WO PCT/US97/176
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APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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NAME/KEY:
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                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCAGGCCCTGCTGACGCTCCAGACTCCG 1920	1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTCTT	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560	1321 AGCCGGTGTCTGTGCCCGGGAAAAGCCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGAAGAA 1380	1141 GACCAPCTTTCTGGGTTCCAGGCCCTGGATGCAGGACTCCCCGCAGGTTGCCCCGCCT 1200	GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1
CGGCTTCAAGGCTGGAGGACACATTTTTCCTGGCGTCATCTCTGACACGGCTCCCT	2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAAGCTCTTTGGGGGTGCTCTTGGGGTGAAGTG 2821 GCCGGCCCACGGCCTATTCCCCTGTAGAAGACGACGCCTGGGTGGATACCCGGACCCTTGGTCAGAT 2821 GCCGGCCCACGGCCTATTCCCCTGGTGGGCCTGCTGCTGGATACCCGGACCCTTGGAGGT	2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGAACTGCGACGGAAAACAACCTCACCCTCACCCTACGCGAAAAACAACCTGTTTGTGGGGGATTTGGTGGATAAACTTTCTTGTTGGTGACACCTCACCCTACCCCACGCGAAAAACACACCTCACCCTCACCCTACCCCACGCGAAAACACACCTCACCTCACCCTACCCCACGCGAAAACACACAC	CAGCCCTGTGCGAGGACATGGAGGAACAAGCTGTTTGGGGGGATTCGGCGGGAAGGGCCTGAAGGGCCTGAACGAGGATGACGGCCTGAACGAGGATGCCGACGAGGGATGCCGGAGGAGAACAAGCTGTTTGGGGGATTCAGGGGGAAGACCTGTTCAAGGGGATTCAGGGGGATGCACGCCTTCAAGGGGGATGCACGACGCATGAGGGGATCAGGGGGATCAGGGGGATGAGGGGGATGAGGGGGATGAGGGGATCCAGGAGATGAGGGGGATGAGGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGGATGAGGGGGAAGAA	2221 G 2281 T 2281 T 2341 C 2341 C	Qy 2041 CAGCGTGCTCAACTACGAGCGGGGCGCCCCGGCCTCCTGGGGCGCCTCTGTGCTGGG 2100

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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
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Best Local Similarity
Matches 4015; Conserv
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APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
- FILING DATE: 18-APR-1997
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FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
ATTARA ACCIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPUTER: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
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CITY: San Francisco
STATE: California
COUNTRY: United State
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                                                                  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
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/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
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Pred. No. 0;
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US-08-854-050-224

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Sequence 224, Application US/08854050 Patent No. 6261836 GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachi
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen I

APPLICANT: Lingher, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase

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               ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA
                                                                                                                                        GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA
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ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA
                                                          GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGGC
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ADDRESSEE: Townsend and Tomessee: Townsend CITY: San Francisco
STATE: Callifornia
COUNTRY: United States of
ZIP: 94111
                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 6309867el
NUMBER OF SEQUENCES: 225
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APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-OCT-1999
CLASSIFICATION: <Unknown>
IOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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INAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hTRT"

/note= "human telomerase reverse

transcriptase (hTRT) catalytic protein

component"

SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-430-323-224
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Best Local Similarity 100
Matches 4015; Conservative
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REGISTRATION NUMBER: 36,429
REBERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                          GGCTCCCAGCTGCGGCCTACCAGGTGTGCGGGGCCGCCGCTGTACCAGCTCGGCGAC
                                                                          CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT
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2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820	2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGGAGCTTGCGGAA 2760	2641 GCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC 2700	2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCT 2640	2521 CAAGTCCTACGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580	2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520	2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460	2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA 2340	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGGGGCGCGTACGACACCATCCCCCA 2220	2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC 2160	2041 CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 2100	1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040	1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGGCCCTGCTGACGTCCAGACTCCG 1920	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC 1860	1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800	
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3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900	CAGATTOGCCATTGTTCACCCCTCGCCCTGCCTTTGCCTTCACCCCACCACCATCC	G	3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720	CATC	3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAG	GAGO	ACTO	GCTG		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0						GCAGAGCIACTACTACAGCTATIGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG		2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

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541	Oy 481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT	Oy 421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGGGGG	QY 361 GCTGCTGGACGGGGCCCCCGGGGGGCCTTCACCACCACCACGTGCGCAGCTA	Qy 301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGAGGAAGAACGTGCTGGCCTTCGGCTTCGC	OY 241 ACGGCCGCCCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGAAGGAGCTGGTGGC	QY 181 GGACCCGGCGGCTTTTCCGCGCGCGCTGGTGGCCTGGTGTGTGCGTGCGTGGCCTGGGACGC	OY 121 GCGGCTGGCCACGTTCGTGCGGGGCCCCAGGGCTGGGGGCTGGTGCAGCGCGGGGCGGGGGCGGGGGGCGGGGGGGG	OY 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAAGCCACTACCGCGAAGTGCT	1 GCAGCGCTGCGTCCTGCTG 1 GCAGCGCTGCGTCCTGCTG	Query Match 100.0%; Score 4015; DB 3; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps	FEATURE: NAME/KEY: CDS LOCATION: (56). S-09-572-423B-3	SEQ ID NO 3 ; LENGTH: 4015 ; TYPE: DNA ; TYPE: DNA ; ORGANIEM: Homo samiens	FILE REFERENCE: ISPH-0462 CURRENT APPLICATION NUMBER: US/09/572,423B CURRENT FILING DATE: 2000-05-16 NIMBER OF SEO ID NOS: 29	APPLICANT: Brett P. Monia ; APPLICANT: William A. Gaarde ; APPLICANT: Edward Wancewicz . TITE OF INVENTION. A NOTICENCE MODIFIATION OF TERT EXPRESSION	US-09-572-423B-3 US-09-572-423B-3 ; Sequence 3, Application US/09572423B ; Patent No. 6331399 . GRANDAL I INFORMATION.	3961	3961	Qy 3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG	
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1621 GAGCCCAGGGGTTGGCTGTGTTCCGGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	1561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGAACTGCGCTTGGCTGCGCAG 1620			1381 CACAGACCCCCGTCGCCTGCCTGCCCGCCCGCTGCCCCAGGCCTCTGGGGCTCCAGGCA 1500	1321 AGCCGGTGTCTGTGGTGGAGAAACCCCCAGGGTTCTGTGGCAGAGCACCCCGAGGAGGAGGA 1380			1191 GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1081 GCCCTCCTTCCTAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080 1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080	961 GCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCATCCGTGGGCCGCCA 960	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGC 900	781 TGCCCCTGAGCCGGAGCGGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGGAGTGCCAGCCGAAGTCTGCCCTTGCCCAAGAGGCCCAAGGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG 720	TCAGGCCCGGCCCCCCCCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC	541 GGCTCCCAGCTGCGCCACACGCTGTGCGGCCGCTGTACCAGCTCGGCGCTGCCAC 600	

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3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	Qy Db	. 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCT 2640	B &
601	94 44 54	2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGTCCATCCTCTCCACGCTGCTCTC 2580	D 29
541	2	2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520	B 8
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421	, p	2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400	P &
361	4d	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340	B 8
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241	р 53	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGGGGG	B 8
181	dd dd	2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC 2160	B 8
121) B Q	2041 CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGGCCTCCTGGGCGCCTCTGTGCTGGG 2100	B 8
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	\$ dd \$	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	₽ Q
281 GAGAGCACTACTCCAGCTATECCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCG 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	S B 8	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860	pb Qy
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Q	181 GGACCCGGCGGCTTTCCGCGCGCGCTGGTGGCCCAGTGCCTGGTGCGTGC	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGGCGGG	Qy 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGTGCCTCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120	Qy 1 GCAGCGCTGCCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCGATGCC 60	300	; NAME/KEY: CDS; CDS; LOCATION: (56)(3454); LOCATION: (56)(3454); LOCATION: Homen telomerase reverse transcriptase (hTRT) cDNA US-09-128-354-1	(EARLIER NUMBER O SOFTWARE	EARLIER FILING DATE: 1997-11-19 EARLIER APPLICATION NUMBER: US EARLIER FILING DATE: 1997-11-19 EARLIER APPLICATION NUMBER: US	EARLIER EARLIER EARLIER EARLIER	; EARLIER FILING DATE: 1997-08-14 ; EARLIER APPLICATION NUMBER: US 08/915,503 ; EARLIER FILING DATE: 1997-08-14 : EARLIER APPLICATION NUMBER: WO PCT/US97/17618	EARLIER FILING DATE: 1997-05-09 EARLIER APPLICATION NUMBER: US 08/911,312 EARLIER FILING DATE: 1997-08-14 EARLIER APPLICATION NUMBER: US 08/912,951	CURRI EARL EARL	APPLICANT: GETON COLOGIA: APPLICANT: GETON COrporation TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants FILE REFERENCE: 015389-003310US CURRENT APPLICATION NUMBER: US/09/128.354	; Sequence 1, Application US/09128354 ; Patent No. 6337200 ; Patent INFORMATION: - APPLICANT. MOVING GROOG B	SULT 6	3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015 	Qy 3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCTGTGGGTCAAATTGGGGG 3960	OY 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
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2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400 	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCAAGGTCCGCAAGGGCCTTCAAGAGCCA 2340	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220	2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC 2160	2041 CAGCGTGCTCAACTACGAGCGGGCGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 2100 [1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGGCTCTCACCTCGAGGGTGAAGGCACTGTT 2040	1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	1861 GGAAGCAGAGGTCAGGCAGCGTCGGGAAGCCAGGCCCGCCC	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860 	1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800	1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTCGAGCTCAGGTCTTTCTT	1621 GAGCCCAGGGGTTGGCTTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	1561 GCTCTCCCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTGGCTGCGCAG 1620	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560	1441 CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCAGGCCTCTGGGGCTTCCAGGCA 1500	1381 CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACCAGCAGCCCCTGGCAGGTGTA 1440	1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGGGGCCCCCAAGGAGGAGGAGGA 1380 1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCAAGGAGGAGAAGACCCCAGGGCTCTGTGGCGGCCCCCAAGGAGGAGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCAGGAGAAGGAAG
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3421 ACTGCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGGCCGACAGCCAGGCCGA	361 361			181 181	121 121	3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA	3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 		881	821 821	761 761	701	641	581 581	521 521	461	401

Query Match 100.0%; Score 4015; DB 4; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCACCCCCGCGATGCC 60	FEATURE: NAME/KEY: CDS LOCATION: (56). OTHER INFORMATI S-09-675-321-1		CURRENT AFFILIAN NUMBER: 05/03/07/03/07/03/07/03/07/07/07/07/07/07/07/07/07/07/07/07/07/	APPLICANT: Geron Corporation TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune TITLE OF INVENTION: Response to a Telomerase Antigen FILE REFERENCE: 015389-003500PC	sequence 1, Application US/09675321 ; Patent No. 6440735 ; GENERAL INFORMATION: ; APPLICANT: Gaeta, Federico C.A.	RESULT 7 US-09-675-321-1	Qy 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015 Db 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015	QY 3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960 Db 3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960	QY 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAACTTTGGAGTGACCAAAGGTGTG 3900 Db 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAACTTTGGAGTGACCAAAGGTGTG 3900	QY 3781 CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTCGACCTCCACCCAC	OY 3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780	QY 3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720 Db 3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGTCGGCTCCACCCCA 3720	QY 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTGAGGGAGTGTCCAGCCAAGGGCT 3660 Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGGCTTGAGGCCTGAGGGCTGAGGGCTTGAGGGCTGAGGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGGCTGAGGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGGCTGAGGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGGGGGG	OY 3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAG	OY 3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG
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	CCCCCTTGTAGACCCAAGCCAAGCCTTCTCCTCTACTCCTCAGGGGCACAAGGAGAGGCTTGTCC	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGA 900 CACCTCTTTGGACCGCTCTCTGGGACGCGCCACCCACCCA	781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGGCAGTCCCAGCCGAAGTCTGCCCTTGCCCAAGAGGCCCAAGACGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG 720	601 TCAGGCCCGGCCCCCCCACACGCTAGTGGACCCCCGAAGGCGTCTGGGATGCGAACGGGC 660	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC 600	481 CCGCGTGGGCGACGTGCTGGTTCACCTGCTGGCACGCTGCGGCGCTCTTTGTGCTGGT 540	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGGCTGCTGCG 480	361 GCTGCTGGACGGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360	241 ACGGCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCAGGCGCCCCCGAAGGAGCTGGTGGC 300	181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGC	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCT	61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGGAGGTGCT 120

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	2221 GG 	2161 GC 2161 GC	2101 CC 2101 CC	2041 CA 2041 CA	1981 CJ 1981 CJ	1921 CT 	1861 GO	1801 CF	1741 TO	1681 C# 1681 C#	1621 G/ 	1561 GC	1501 C	1441 CC 1441 CC	1381 Q 1381 Q	1321 A 1321 A	1261 G		1141 G
	ACAGGCTCACGGAGGT	GCCTGAGCTGTACTT	IGGACGATATCCACAC IGGACGATATCCACAC	GCGTGCTCAACTACGF	GAACGTTCCGCAGAG <i>F</i> GAACGTTCCGCAGAG <i>F</i>	rcatccccaagcctg/ rcatccccaagcctg/	nagcagaggtcaggc <i>i</i> nagcagaggtcagg <i>ci</i>	agttgcaaagcattgc agttgcaaagcattgc	TCACGGAGACCACGTT	AGTTCCTGCACTGGCT	GCCCAGGGTTGGCTC 	TCTCGCTGCAGGAGC	ACGAACGCCGCTTCCT	ectrogradascon ctrogradascon	CAGACCCCCGTCGCC	ccggrercrgrecco	GCCCCTACGGGGTGC GCCCCTACGGGGTGC	CCCAGCGCTACTGGC CCCAGCGCTACTGGC	CCATCTTTCTGGGTT
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	DAAACCCCAGAACACG	BACGGGCGCGTACGAC 	erecrecererecee	GGCCTCCTGGGCGCC	CTCACCTCGAGGGTG CTCACCTCGAGGGTG	rgtgaacatggactac rgtgaacatggactac	SCCGCCTGCTGACG	GAAGAGGGTGCAGCTG	CTTTTTCTACCGGAAG 	CGTCGAGCTGCTCAGG	GCACCGTCTGCGTGAG	CGTGCGGGACTGCGCT CGTGCGGGACTGCGCT	GTTCATCTCCCTGGGG 	gccccaggccrcrgg 	CCAGCACAGCAGCCCC	CTCTGTGGCGGCCCCC	cccgcTgcgAgcTgcg cccgcTgcgAgcTgcg	TCTGGAGCTGCTTGGG TCTGGAGCTGCTTGGG	
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Patent No. 6444650
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                        APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                       COUNTRY:
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Best Local Similarity
Matches 4015; Conserv
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PRIOR APPLICATION DATA:
APPLICATION WHEER: US 08/911,312
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997

PRIOR APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WS 08/974,584
FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
COTHER INFORMATION: /product= "human telomerase
OTHER INFORMATION: transcriptase (hTRT)"
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 25-APR-
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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PRIOR APPLICATION UDATA:
APPLICATION UDMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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; Pred. No. 0;
0; Mismatches
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CAGGGGTACTGGCAATGGGGGCCCAGCCAGCCAGCCATGTTTTTTCTGGGTTACTCAGTGCCAACCAA		GCGGGGGGCAGGCAGGGGAGGGAGGGAGGGAGGGAGGGA	CCAACTGGGGGACCAACCACGACCACACACGGTGACCGACGGGGGGACGACGACGACGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	CTGGCCACGTTCGTGCGCGCCTGGGGGCCCTGGGGGGCCTGGGGGGCCTGGGGGCCTGGTGG
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2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG

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CCATTGITCACCCCTCGCCCTGCCCTTCCTTTCCACCCCCACCATCC 3840
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US-08-912-951-1
; Sequence 1, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: HOWENTION: THERAPEUTIC METHODS
UNMBER OF INVENTION: THERAPEUTIC METHODS
UNMBER OF INVENTION: THERAPEUTIC METHODS
UNMBER OF INVENTION: THERAPEUTIC METHODS
UNMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STREET: California
COMPUTER CALABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435

DIAGNOSTIC AND

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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TIMPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: APDIC, RANGOLD T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: limolecule Type: FEATURE:
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LOCATION: 56..3454
OTHER INFORMATION:
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/note= "human telomerase reverse
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                                                                                                                                               AGCCGGTGTCTGTGCCCGGGAGAAGCCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA
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1621 GCTCTGCGTGCGGGGTTGCTTTTTTCTACCGGAACACTTGCGCTGGGGGGGG	GGGGAAGCAI . GGGAAGCAI
2701 CTTCCTCAGAACCCTTGTCCGAAGTGTCCCTTAGATATGGCTTGCGTGATATATTGCGGAAACTTCCGAAACTTCCGGAAACTTCCGGAAACTTCCGGAAACTTCCTGGAACACTTCCGGAAACTTCCTGGAACACTTCCGGAAACTTCCTGGAACACTTCCGGAAACTTCCAGATTTCCCTGGAAAAACACAGACCCTTGGATGACACGGCCTTTTGTTCAAATTCCCTGGAAACAACAGACCCTGCAGATTCCCCTGGATGACCAGGCCTTCAACTTCCAGCTTTGTTCAAATTCCCCTGGAACAACTACTTCCAGCTTAAACCTGGAACCTTCCAACTTCCAGCTTAAACTTCCAGCTTAAACTTCCAGCTTAAACACAGACCTTCCAACTTCCAGCTTCAACCTCAACCT	Qy 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCT 2640

ACGGCCGCCCCCGCCGCCCTCCTTCCGCCAGGTGTCCTGCCTG	181 GGACCCGGCGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGGCGTGCCTTGGGACGC		4 —4	CTGGCCCCGGCACCCCGCGATGCC 60	Query Match 100.0%; Score 4015; DB 4; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	:	; SEQ ID NO 3 ; LENGTH: 4015 ; TYPE: DNA ; ORGANISM: Homo sapiens	; CURRENT FILING DATE: 2000-12-07 ; PRIOR APPLICATION NUMBER: 09/572,423 ; PRIOR FILING DATE: 2000-05-16 ; NUMBER OF SEQ ID NOS: 108	; APPLICANT: Edward V. Wancewicz ; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION ; FILE REFERENCE: ISPH-0527 ; CURRENT APPLICATION NUMBER: US/09/733,294A	; GENERAL INFORMATION: ; APPLICANT: Brett P. Monia ; APPLICANT: William Gaarde ; APPLICANT: Susan M. Freier	RESULT 10 US-09-733-294A-3 ; Sequence 3, Application US/09733294A ; Patent No. 6492171				Db 3781 CCAGATTCGCCATTGTTCACCCCTCGCCTGCCCTGCCTTTGCCTTTCACCCCCACCCA	Db 3721 GGGCCAGCTTTTCACCAGGAGCCCGGCTTCCACCACATAGGAATAGTCCATCC 3780 QY 3781 CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTTGCCTTTCCACCCCCCCC	Db 3661 GAGTGTCCAGCACACACCTGCCGTCTTCACTTCCCCCACAGGCTGGCGCTCGACCCCA 3720 OY 3721 GGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780	
Qy 132 Db 132 Qy 138	Qy 1:	Ωy 1;	ОУ 1: 1:	. Db 11	Оу 1 Db 1	D Qy	Db Qy	Db Qy	dg Vg	Db Qy	QV db	Qy dd	Qy Db	Qy Db	D Q	ДУ	Db	γQ
.321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAGGAGGAGGAGAGAGA	261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGGCTGCGAGCTGCGGTCACCCCAGC 1320	201 GCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260	1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT 1200	1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080 	961 GCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020	901 CACCTCTTIGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA 960 	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGGCCGAAGAAGC 900 	781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGGAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAGGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCCGGGTGCGAG 720	601 TCAGGCCCGGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGTGCCAC 600	481 CCGCGTGGGCAACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCGC	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGCGGGGGGGG	361 GCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCAGCGTGCGCAGCTA 420	01 CCGAGTGCTGCAGAGGCTGTGCGAGGCGCGGGGGGGGGG	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGGC 360

461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 25	2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460	2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400	TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA	garlaggetlacgaaggtrategecageateateaaacecelagaacacgtactgegegegegegegegegegegegegegegegegegege	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGGGGG	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGGTGTGCGGGCCCAGGACCC	2041 CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 2100	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	1921 CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	GGAAGCAGAGGTCAGGCAGCATCGGGAAAGCCAGGCCCGCCC		1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800 	1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTCTT	1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	1561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTGGCTGCGCAG 1620	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560 	1441 CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTTCCAGGCA 1500	
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3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAG		ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 34	GCTGAGTCGGAAGCTCCCGGGGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGGC 34	3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360	CGGCCTCTGCCCTCCGAGGCCGTGCAGTGGCTTGCCACCAAGCATTCCTGCTCAAGCT	CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCCAGGGCCCCGC	3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180	CAAGATCCTCCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 31	3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060	2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000 [2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGACCGACTCTCACCTTCAACCG 2940	GCCGGCCACGGCTATTCCCCTGGTGCGGCTGCTGCTGGTACCCGGACCCTGGAGGT 	ACAGTGGTGAACTTCCCTGTAGAACGACGACGCCTGGGGGCGCTTTGTTCAGAT 2	CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGGGTGGTGAACTTGCGGAA	41 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGAAAC 270	CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT	CAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCTG 2	

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RESULT 11
US-09-402-181B-1
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GENERAL INFORMATION:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/99/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/951,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chapman, Aregg B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
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Nakamura, Toru
Chapman, Karen B.
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Best Local Similarity
Matches 4015; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protei
component"
                                       GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC 600
                                                                                                                                                                          GCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420
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                                                                                                                 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGCGGGGGCTGGGGGGCTGCTGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	21 GAGCCCAGGGGTTGGCTTCCCGCCGCCGCCGCACACCGTCTGCGTGAAAATCCTGGC 168		CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCL	1441 CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA 1500	81 0	1 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGAAGACGA 13	132 132	GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 126	accarctttctgggttccaggccctggargccagggactccccgcaggttgcccggct 120	GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 11	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080	GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1	O1 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	41 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCGGCGAAAAAGC 90	TGCCCCTGAGCCGGAGCGGACGCCCTTGGGCAGGGTCTGGGCCACCCGGGCAGGAC 8	1 GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCCATGCCCAAGAGGCCCAGGCGTGGCGC 78	61 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCCAGCCCCGGGTGCGAG 72	601 TCAGGCCCGGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGC 660
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GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2	2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGGTGGAACTTGCGGAA 2760	2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGAAAAC 2700	81 CAGCCTGTGCTACGGCGACACTGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT 	21 CAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTTCCACGTGCTGCTGTGTTGTGTTGTTGTTGTTGTTGTTGTTGTT	61 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACGCCGTGCGCATCAGGG 252	1 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCCAGAACACGTACTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGGGGTACGACACCATCCCCCA 2220	2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC 2160	1 CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCCTCTGTGCTGGG 	CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 	1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 	1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800 	1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT

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AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG
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Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
TELEPHONE: (415) 576-020
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY AGENT INFORMATION:
                                                          NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and
STREET: Two Embarcadero
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IOR APPLICATION UNMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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STATE: California
COUNTRY: USA
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Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
OF INVENTION: Human Telomerase Catalytic Subunit
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Nakamura, Karen B.
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Center, Eighth Floor
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NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-721-456-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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                      GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAGAGGCCCAGGCGTGGCGC
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                                                                                      GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCCTGCGCAG
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3960	ACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG	3901	뮍
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3900	AGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG	œ	Д
3900	AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTTGGAGTGACCAAAGGTGTG	84	Ş
3840	CAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCCACCATCC	, 3781	ఠ
3840	CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTCCTT	3781	ş
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3780	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCCACATAGGAATAGTCCATCC		γ
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3660	CATGTCCGGCTGAAGGCTGACGTGTCCGGCTGAGGCCAAGGGCT		дb
3660	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT	3601	Ş
3600	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTTGGCCGAGGCCTG	3541	Дb
3600	PAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTTGGCCGAGGCCTG	3541	Ş
3540		3481	Dр
3540	CAGGGAGGGAGGGGCGCC		γQ
3480	CCCCACACCCAGGCCA	3421	망
3480	TCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA	4	Ş
3420	CGCAGCCAACCCGGC	3361	Db
3420	GCTGAGTCGGAAGCTCCCGGGGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC	ũ	Ş
3360	GTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA	3301	ф
3360	CGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA	3301	Ş
3300	CCACCAAGCATTCCTGCTCAAGCT		Дb
3300	CCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT		γŞ
3240	CGC	3181	Дb
3240	CTACTCCATCCTGAAAGCCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGC		δ
3180	CCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT	3121	дb
3180	AGCAAGTTTGGAAAGACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT	3121	γQ
3120	CAAGATCCTCCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA	90	90
3120	CTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTÇA	3061	VQ.
	TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3001	Дb
3060	CAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3001	Ş

RESULT 13 US-09-953-052-1 ; Sequence 1, Application US/09953052 ; Patent No. 6627619

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ULIBER INFORMATION: /product= "human telomerase; transcriptase (hTRT)"; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-953-052-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 01
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FILING DATE: 14-Sep-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
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                                                                                                                                          TOPOLOGY:
                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/052,919
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-WAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/9511,312
                                                                                                                                                                             LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                             NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION:
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                                                                                                      NAME/KEY:
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
Andrews, William H.
Inhibiting Telomerase Reverse Transcriptase
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301 CCGAGTGCTGCAGAGCTGTGCGAGCGCGGAGGAAACGTGCTGGCCTTCGGCTTCGC 360	301 CCGAGTGCTGCAGAGGCTGTGCGAGGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360	241 ACGGCCGCCCCGCCGCCCCTCCTTCCGCCAGGTGTCCTGCCTG	241 ACGGCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	181 GGACCCGGCGGCTTTTCCGCGCGCGCTGGTGGCCCAGTGCCTTGGTGTGCGTTGCCCTGGGACGC 240	181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGCTGGCACGC 240	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCCAGGGCTGGCGCGGTGCAGCGCGG 180	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180	61 GCGCCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACCTACCGCGAGGTGCT 120	61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTGCCTGCGCACTACCGCGAGGTGCT 120	1 GCAGCGCTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCCGCGATGCC 60	1 GCAGCGCTGCGTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCCGCGATGCC 60	Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%;

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041 CAGCGTGCTCAACTACGAGCGGCCGCGCGCCCCGGCCTCCTGGGCCCCCTGTGCTGGG 2100	921 CITCATCCCCANGCCIANCGGCIGCCGATIGICACTICACCICGIGGGCCIGGGGGCCIAGGGCCCICGGGGGCCCIGGGGGCCIGGGGGCCIGGGGGGG	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCCCCTGCTGACGTCCAGACTCCG 19	1 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 18 	1 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAAGAGTGTCTGGAG 1 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAAGAGTGTCTTGGAG 1 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAAGAGTGTCTTGGAG	1 CAAGITCCTGCACTGGCTGATGAGTGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT	1 GAGCCCAGGGGTTGGCTGTGTTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGAGATCCTGGC 16	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG 16	1 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 15	.441	1 CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCAGCAGCAGCCCCTGGCAGGTGTA 144		261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC 1320	201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260	41 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCAGGTTGCCCCGCCT 1200	.081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
OY 3121 TCAGCAAGTTTGGAAACCCCACATTTTTCTGCGCGTCATCTTGACACGCCTCCCT 3180 Db 3121 TCAGCAAGTTTGGAAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180 OY 3181 CTGCTACTCCATCCTGAAAGCCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCGCCGC 3240 OY 3181 CTGCTACTCCATCCTGAAAGCCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCGCC 3240	3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACCA	Qy 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTGAAGTG 3000 Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTTGGGGTCTTGCGGCTGAAGTG 3000 Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTTGGGGTTGCAGCTGAAAGTG 3000 Qy 3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCGTCTAGACGGTGTGCACCAAACATCTA 3060	2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	Qy 2821 GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGCTGGATACCCGGACCCTGGAGGT 2880	Qy 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820	Qy 2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGGTGAACTTGCGGAA 2760	Qy 2641 GCTCCTGCGTTTGGTGGATTATTCTTGTTGGTGACACCTCACCCCACGCGAAAAC 2700	OY 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGACGGGCT 2640	Qy 2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGCTCCATCCTCTCCACGCTGCTCTG 2580	1 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG	OY 2401 GACCAGCCCCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460	41 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACACHTTCGTGGCTCACCTGCAGGA CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2281 2281	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATACCCCAGAACACGTACTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGGGTACGACACCATCCCCCA 2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA	2101 COTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGTGC

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Sequence 1, Application US/09465491

Pateent NO. 6664046

GENERAL INFORMATION:
APPLICANT: Chang, Sheng-Yung P.
APPLICANT: Santini, Christopher D.
TITLE OF INVENTION: Quantitation of hTERT mRNA EXF
FILE REFERENCE: RRANO02
CURRENT APPLICATION NUMBER: US/09/465,491
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
CRGANISM: Homo Bapiens
US-09-465-491-1
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Best Local Similarity
Matches 4015; Conserv
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        GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCCGTTGCCCAAGAGGCCCCAGGCGTGGCGC
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                                            100.0%; Score 4015; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Tede
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
                                                                                                                                                                             Matches
                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-NOV-CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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Pred. No. 0;
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RESULT 15 US-08-974-549A-343

Sequence 343, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:

APPLICANT: Cech, Thomas APPLICANT: Lingner, Joac APPLICANT: Nakamura, Tor APPLICANT: Chapman, Kare

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco

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AGGTGCTGT AGGTGCTGT	CCTGTACAC	GTGGAGAC GTGGAGAC	CAGATTCGC CAGATTCGC	GCCAGCTT GCCAGCTT	AGTGTCCAG AGTGTCCAG	ATGTCCGGC	ACACCCAGG ACACCCAGG	AGCAGACAC	TGCCCTCAC	TGAGTCGG
GGAGTAAA GGAGTAAA	AGGCGAGGA AGGCGAGGA	CCTGAGAAG CCTGAGAAG	CATTGTTCA CATTGTTCA	TTCCTCACC	CACACCTGO CACACCTGO	TGAAGGCTG.	CCGCACCG	CAGCAGCCC CAGCAGCCCC	BACTTCAAG BACTTCAAG	AAGCTCCCG
GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015 	CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG	AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTTGGAGTGACCAAAGGTGTG 	CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCACCATCC	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAG	GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC
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TTTCAGTTT TTTCAGTTT	GTCCCTGTG	AATTTGGAG AATTTGGAG	TTTGCCTTC	CCCCACATA CCCCACATA	GGCTGGCGC	GAGCGAGTG GAGCGAGTG	AGTGAGTGI AGTGAGTGT	GTCCCAGGG GTCCCAGGG	CCACCCGCC	CTGGAGGCC
TGAAAAAA : TGRAAAAA	GGTCAAAT GGTCAAAT	TGACCAAA TGACCAAA	CACCCCA	GGAATAGTO GGAATAGTO	TCGGCTCQ	TCCAGCCAJ TCCAGCCAJ	TTGGCCGAC	;agggaggg ;agggaggg	CACAGCCAC	GCAGCCAA
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Search completed: October 30, 2004, 03:18:16 Job time : 321 secs

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-Q=/Ggn2_1/USPTO_Spool/US10044652/runat_28102004_103655_1383/app_query.fasta_1.1287
-DB=Issued_Patesits_Na -QFMT=fastap_SUFFTX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_WIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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US-09-721-456-639

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            FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMAT
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Worin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/974,549A FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
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US-09-402-181B-1
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US-09-465-491-1
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US-09-402-181B-343
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US-08-974-549A-29
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Query Match: ..
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PILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION: 18FORMATION:
TELECOMMUNICATION 18FORMATION:
TELECHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
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STRANDEDNESS: single
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 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
                              GATGCGCGCCGCCGGCGGCGCCGAGCTTTCGCCAGGTGAGCTGCCTGAAAGAACTG
                                               AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu
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alternative codon distributions for
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                                                                                                                      AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr
                                                                                                                                                               CGCCTGCCGCAGCGCTATTGGCAGATGCGCCCGCTGTTTCTGGAACTGCTGGGCAACCAT
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TGTGAGCACCTGACCGATCTGAGCGCCGTATATGCGCCAGTTTGTGGGCGC	ValargargTyralaValValGlnLysalaAlaHisGlyHisValargLysalabheLys 7	AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	51 LeuPheserValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680	1 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640	11 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600	11 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560		nGluargargPheLeuargAsnThrLysLysPheIleSerLeuG; 	21 GAAGATACCGATCCGCGCCGCCTGGTGCAGCTGCTGCGCCAGCATAGCAGCCCGTGGCAG 1380 1 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
US RE	Q & Q	Qy Qy	B & B &	D Q D 4	5 B B B 1	S B S B	Q B Q B	QY QY	Qy Db
49A-639 639, Application US/08974549A 636178 INFORMATION: ANT: Cech, Thomas R. ANT: Lingner, Joachim ANT: Nakamura, Toru	1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120	1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080	1021 PheH18GINGINVALITY DIXBASH PROTITE PHE LEUKTGVALL LES ELAB PINTALA 1040			GINMet ProA	2581 ĠĠĊĊĠĠĊĠĠĊĠĠĠĠĊĠĠŦĠĠŦĠĀŦĠŦŦŦŦĊĠĠŦĠAĊĊĊĠĊAŦĊŦĠAĊĊĊAŦĠĊĠ 2640 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900	841 LeuCysSerLeuCysTyrGlyAspMetGluAardLysLeuEneAlaGlyIleAkgArgAsp 860	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR DATE: 01-OCT-1996
PRIOR DATE: 01-OCT-1996
PRIOR DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 25-APR-1997

PRICK APPLICATION NUMBER: US 08/851,843

PILING DATE: 06-MAX-1997

PRICK APPLICATION NUMBER: US 08/854,050

PILING DATE: 06-MAX-1997

PRICK APPLICATION NUMBER: US 08/854,050

PILING DATE: 09-MAX-1997

PRICK APPLICATION NUMBER: US 08/911,312

PILING DATE: 14-AUG-1997

PRICK APPLICATION NUMBER: US 08/912,951

PRICK APPLICATION NUMBER: US 08/912,951

PRICK APPLICATION NUMBER: US 08/912,951

PRICK APPLICATION NUMBER: US 08/915,503

PRICK APPLICATION NUMBER: US 08/915,503

PRICK APPLICATION NUMBER: WG DATE: 14-AUG-1997

PRICK APPLICATION NUMBER: WG DATE: 14-AUG-1997

PRICK APPLICATION DATA:

APPLICATION NUMBER: WG DATA: 14-AUG-1997

PRICK APPLICATION DATA: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 639:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO POFILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO POFILING DATE: 01-OCT-1997
NAME/KEY: - 1.3396
LOCATION: 1.3396
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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APPLICATION NUMBER: US 01
PILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
APPLICATION NUMBER: US 01
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                         EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Te
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                            OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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TITLE OF II
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TOPOLOGY: linear
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CITY: San
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T: Morin, Gregg B.
T: Harley, Calvin B.
T: Andrews, William H.
INVENTION: Human Telomerase Catalytic
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genes)"
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Best Local Similarity:
Query Match:
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ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro
                                              GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
                                                                                                ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu
                                                                                                                                     GGTGCTGCTCCGGAACCGGAACGTACCCCGGTTGGTCAGGGTTCCTGGGCTCACCCGGGT
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Matches:
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LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680	GlyAlaArgThrPheArgArgGluLy8ArgAlaGluArgLeuThrSerArgValLy8Ala 660	1920	1860	u 600 	561 PheTyrValThrGluThrThrPheGlnLy8AsnArgLeuPhePheTyrArgLysSerVal 580	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560	e 540 	u 520 G 1560	8 500 - C 1500	ArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480	1380	u 440 A 1320	r 420 C 1260	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis 400	o 380 	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360	321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340	
Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040	Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020	Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000	961 ABRARGGIYPheLYSAlaGIYARGASRMetArgArgLySLeuPheGIYValLeuArgLeu 	941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 	Oy 921 GINMETPIOALAHISGLYLEUPHEPFOTTPCYSGLYLEULEULABPTHTAGTHTLEU 940	901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900	Qy 861 GlyLeuLeuLeuArgLeuVelAspAspPheLeuLeuVelThrProHisLeuThrHieAla 880	Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860	Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840	801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIIe 	Qy 781 GlnGluThrSerProLewArgAspAlaValValIleGluGlnSerSerSerLewAsnGlu 800	Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780	Oy 741 ValArgArgTyrAlaValValGInLysAlaAlaHisGlyHisValArgLysAlaPhoLys 760	721 ProGlaAspArgieuThrGluValIleAlaser1leIleLysProGlaAspThrTyrCys 7	701 AspProProProGluLeuTyrPneVally8VallAspValThrGlyAlaTyrAspInTile (2041 CTGGGTCTGGACGACCGTGCTTGGCGTACCTTCGTGCGTG	1981 CT

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN PC-DOS/MS-DOS
SOPTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/724,643
PILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION
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APPLICANT:
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APPLICANT:
                                                                                                                         PILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                             FILING DATE: 25-APR-PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                             FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
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                                                                                                      APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
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Two Embarcadero Center, Eighth Floor
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
Andrews, William H.
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25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.30
                                                   US 08/912,951
                                                                                                                                                                                                                                                                                     US 08/851,843
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-044-692-2 (1-1132) x US-08-974-549A-640 (1-3396)
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INFORMATION FOR SEQ ID NO: 64
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGCTAGACCACCAGCTGCTCCATCTTTTAGACAAGTTTCTTGTTTGAAAGAATTG
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                                                                                                                                                                                                    SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
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                                                                                      LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
                                                                                                                                                            TCTTATTTGCCAAATACTGTTACTGATGCTTTGAGAGGTTCTGGTGCTTGGGGTTTGTTG
{\tt LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlar}
                                                        TTTGCTTTGTTTGGATGGTGCTAGAGGTGGTCCACCAGAAGCTTTTACTACTTCTGTTAGA
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alternative codon distributions for
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1501 GCTAAATTGCTTTGCAAGAATTGACTTGGAAAATGTCTGTTAGAGATTGTGCTTGGTTG 1560 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540	1441 AGACATAATGAAAGAAGATTTTTGAGAAAATACTAAAAAATTTATTT	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460 	421 ProAlaAlaGlyValCysAlaArgGluLysBroGlnGlySerValAlaAlaProGluGlu 440 	401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420 	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400 	361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380 	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360 	321 CYBProDroValTyrAlaGluThrLysHisBheLeuTyrSerSerGlyAspLysGluGln 340 	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320 	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 .	261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280 	241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260 	221 AlaargArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240 	201 ArgalaTrpasnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220 	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgAsgLeuGlyCysGlu 200 	
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9	ę Q	당 성	B 8	, B &	, B 2	S B 8	, B &	, B &	S & &	S B &	5 B Q	p &	5 A	B &	, B &	. B &	B	& B
2581 GGTTTGTTGTTGAGATTGGTTGATGATTTTTTGTTGGTTGCTCCACATTTGACTCACACCACACCACACCACACCACACCACACCACACCAC	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 88	841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheA.laGly1leArgArgAsp 860	ATGGLYDYSSELTYFRATGLICYSGLIGGYSLIFECGELIGEGGELIGUEGGELIGUEGGELIGUEGGELIGUEGGELIGUEGGELIGUEGGELIGUEGGELIGUEG	OI ALASETSETCLY MENTENABY ALTRIBUTATION OF THE TRANSPORT		761 SETHISVALSETINTHEUNINTASPHEUDINFTOTYNTEURINFTOTYNTUTYNTUURINFTOTYNTUURINFTOTYNTUURINFTOTYNTUURINFT	ValargargTyralavalvalGlnLyBalaAlaHl8GJyHl8ValArgDyBalarneLy8				LeupheservalueuAsmiyrGiuArgAlaArgArgeroGiyeGueuGusyAlaservalueuAsmiyrGiuArgAlaArgArgeroGiyeGueuGusyAlaservalueuAsmiyrGiuArgAlaArgArgeroGiyeGueuGusyAlaservalueuAsmiyrGiiTiTiTiTiTiTiTiTiTiTiTiTiTiTiTiTiTiTi	1 GIYALAANGINIFNIGATGATGATGATGATGATGATGATGATGATGATGATGATG	21 LeuArgpheILeProLy8ProAspG1YLeuArgpro1LeValAsmmetAsp1YrValVal 64	ol redsers lunalas lunalas germanas germanas germanas elementes el le	1 IDSELD/SUGUSINSELTICON/YICANAS CAN Y CALUMINAS CONTROL Y CALUMINAS CAN Y C	1 FREST TWO CONSTRUCTS CONTINUE TO THE PROPERTY OF THE PROPERT	21	1561 AGAAGATCTCCAGGTGTTGGTTGTGTTCCAGCTGCTGAACATAGATTGAGAGAAGAAATT 1620 541 LeuAlaLysPheLeuHisTTpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560

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US-08-974-549A-641
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 641, Application US/08974549A Patent No. 6166178
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                       STREET: I'WO CITY: San Francisco
STATE: California
                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                    PPLICANT: Lingner, Joachim
PPLICANT: Nakamura, Toru
PPLICANT: Chapman, Karen B.
PPLICANT: Morin, Gregg B.
PPLICANT: Harley, Calvin B.
PPLICANT: Andrews, William H.
PPLICANT: Andrews, William H.
                                                                                  COUNTRY:
                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGCTTTGCCATCTGATTTTAAAACTATTTTGGAT 3396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTGACTAGACATAGAGTTACTTATGTTCCATTGTTGGGTTCTTTGAGAACTGCTCAA
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                                                                                                                                                   E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                          Thomas R.
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                                                                                                                 US-10-044-692-2 (1-1132) x US-08-974-549A-641 (1-3396)
                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 14-AUG-:
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FILING DATE: 18-APP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US OFFILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 14-AUG-:
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PRIOR APPLICATION DATA:
US
                                                                                                                                                                                                                                                                                                                             LOCATION: 1..3396
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
                                                           MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
                                       ATGCCAAGAGCTCCAAGATGTAGAGCTGTTAGATCTTTGTTGAGATCTCACTACAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3396 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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n Release #1.0, Version
                                                                                                                                                                                                                                                                                                                             /note= "hTRT-encoding sequence employing
alternative codon distributions for
yeast (high expressing genes)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO PCT/US97/17618
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                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                         Conservative: Mismatches:
                                                                                                                                                                       Indels:
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ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 4	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360	321 CÝSProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340 	ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	GlualaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	ArgThrargGlyProSerAspargGlyPheCysValValSerProAlaArgProAlaGlu 	GIYAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLyBArgProArgArg 2 	ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 	LeuValAlaProSerCyaAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 	LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 	SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 1 	PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 	ValAlaargValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 	61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80	41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60 	
Qy 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760 .	Qy 721 ProGlnAspArgLeuThrGluVallleAlaSerIleIleLysProGlnAsnThrTyrCys 740	701 ABPPTOPTOGIULEUTYYPDEVAILYSVAITASJVAITATGJVAIATYTASPTATILE	681 LeuGlyLeuAspAspIleHsaArgAlaTrpArgThrPheValLeuArgValArgAlaGln	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 	Qy 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660	Qy 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640	Oy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620	Oy 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600	Qy 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580	Qy 541 LeuAlaLysPheLeuHisTTpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560	Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540	Qy 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520	Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500	Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480	Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460	OY 421 ProAlaAlaGlyValCysAlaArgGluLysErOGINGLYSErValAlaAlaProGluGiu 440	1201 GCTCAATGTCCATACGGTGTTTTGTTGAAGACTCACTGTCCATTGAGAGCTGCTGTACT	1141

1120 3360	1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 	
1100 3300	81 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlac 	
1080 3240	061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeu 	
1060 3180	041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLys 	
1040 3120	021 PheHisGinGinValTrpLysAsnProThrPhePheLeuArgValIleSerAspT\ 	
1020 3060	001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheH: 	
1000	981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnS 	
	1 AsnargGlyPheLysAlaGlyArgAsnMetArgArgLysL 	
960 2880	41 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaS	
940 2820	1 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeu	
920 2760	01 ArgLysThrValValAsnPheProValGluAspGlu 	
900 2700	81 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAs 	
880 2640	61 GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 	
860 2580	1 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 	
840 2520	21 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 	
820 2460	heMetCysHisHisAlaValArgIle CATGTGTCACCACGCTGTTAGAATT	
800 2400	81 GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 	
780 2340	61 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPh 	

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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
STATE: California
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GENERAL INFORM
APPLICANT:
APPLICANT:
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COMPUTER: IM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                     APPLICATION UNMER: US 08/851,843
APPLICATION UNMER: US 08/854,050
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
PRILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
PREFERENCE/NOTUSE NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 642:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Nakamura, Toru
Chapman, Karen B.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION:
OTHER INFORMATION:
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                    TIGGTIGCCCCATCTIGTGCCTACCAAGTTTGTGGTCCACCATTGTACCAATTGGGTGCC
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                                TrpSerLysLeuGl
                                               PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal
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GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla
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                                                                     AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu
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US-09-721-456-638
; Sequence 638, Application US/09721456
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; GENERAL INFORMATION:
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                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Vere
CURRENT APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION VUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-RPR-1997
APPLICATION NUMBER: US 08/844,617
FILING DATE: 18-RPR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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        APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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LOCATION: 1.3396

OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for E. coli (all genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 638:
US-09-721-456-638
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REGISTRATION NUMBER: 36,429
REFERENCE/DOKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
                                                                                                                                                                 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
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TYPE: nucleic acid
STRANDEDNESS: single
                                              SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
                                                                                                                                                GTGGCGCGTGCTGCAGCGCCTGTGCGAAACGCGGCGCGAAAAAACGTGCTGGCGTTTGGC
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                                              CGCCATAACGAACGCCGCTTTCTGCGCAACACCAAAAAAATTTATTAGCCTGGGCAAACAT
                                                             ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis
                                                                                                        GIGTATGGCTTTGTGCGCGCGTGCCTGCGCCCGCCTGGTGCCGGCCTGTGGGGCAGC 1440
                                                                                                                        GAAGATACCGATCCGCGCCGCCTGCTGCAGCTGCCGCCAGCATAGCAGCCCGTGGCAG 1380
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AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle
                                                                  GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla
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US-09-721-456-639
; Sequence 639, Application US/0972
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Cata
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townser'
STREET: Two Embarcadero Cent
CITY: San Francisco
STATE: California
COUNTRY: USA
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Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40 	Oy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20	US-10-044-692-2 (1-1132) x US-09-721-456-639 (1-3396)	100.00%	es:	ent Scores: No.:	SEQUENCE DESCRIPTION: SEQ ID NO: 639: US-09-721-456-639	OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for enteric bacteria (high expressing	MOLECULE TYPE: DNA ; FEATURE; ; RAME/KEY: -	TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear		TELEPHONE: (415) 576-0300	NAME: Apple, Randolph Ted , REGISTRATION NUMBER: 36,429 , REFERENCE/DOCKET NUMBER: 015389-002610US TELECOMMINICATION INFORMATION:	; APPLICATION NUMBER: WO PCT/US97/17885 ; FILING DATE: 01-OCT-1997 ; ATTORNEY/AGENT INFORMATION:	APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997		ATION :	; RILING DATE: 05-MAX-1997 ; APPLICATION NUMBER: US 08/854,050 ; EILING DATE: 09-MAX-1997	FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/851,843	; APPLICATION NUMBER: US 08/844,419 ; FILINGE 18-APR-1997 APPLICATION NUMBER: US 08/846.017		; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/08/974,549A ; FILING DATE: 19-NOV-1997	APPLICATION UMMER: US/09/721,456 FILING DATE: 22-No. 6617110-2000 CLASSIFICATION: <unknown></unknown>	OFEKALING SISIEM: FC-DOS/MS-DOS ; SOFTMARE: Patentin Release #1.0, Version #1.30 . CIRDENUM ADDITION DATA.	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	ZIP: 94111-3834
B Q	D 5) (B &	Db	Q !	p} Q	B 8	da Qy	g d	? F	ş Q	DD QY	Db	Q	B &	Db	& 8	ş 8	В	δ	B 8	Db 5	? 5	. Q	망
381 ArgLeuProGIDArgTyrTrpGLnMetArgProLeuPheLeuGILLeuLeuGIYASDH18 400		**	341 LeuArgProSerPheLeuLeuSerSerLeuArgProErLeuThrGlyAlaArgArgLeu 360	961 TGCCCGCCGGTTTACGCTGAAACCAAACACTTCCTGTACTCCTCCGGTGACAAGAACAAG 1020	CysProProValTyrAlaGluThrLysHisPheteuTyrSerSerGlyAspLysGluGln 34	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320 	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 	261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280	78	2 6	21 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	201 ArgAlaTrpAsnHisSerValArgGIuAlaGlyValProLeuGlyLeuProAlaProGly 220 		81 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	161 LeuvalAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180	1 CTGCGTCGTGTTGGTGACGACGTTCTGGTTCACCTGCTGGCTCGGTTGCGCT	ictactactactactactactactactactactactactac	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140	301 TTCGCTCTGCTGGACGGTGCTCGTGGTGCTCGGCGGAAGCTTTCACCACCTCCGTTCGT 360	1 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSe	81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100	GACGCTCGTCCGCCCGCCGGCTGCTTCCGTCAGGTTTCCTGCCTG	Tanalaarabrotrotrotrotrotrotrotrotrotrotrotrotrotr	41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60	61 GTTCTGCCGCTGGCTACCTTCGTTCGTCGTCTGGGTCCGCAGGGTTGGCGTCTGGTTCAG 120

701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720	641 GlyAlaArgThrPheArgAluLysArgAlaGluArgLeuThrSerArgValLysAla 660	581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600	1561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuhepheTyrArgLysSerVal 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuhepheTyrArgLysSerVal 561 PheTyrValThrGluThrThrPheGlnLysAsnArgCrGTTGTTCTTCTACCGTTAAATCCGTT 561 TTCTACGTTACCGAAACCACCTTCCAGAAAAAACCGTCTGTTCTCTACCGTTAAATCCGTT 1681 TTCTACGTTACCGAAACCACCTTCCAGAAAAAACCGTCTGTTCTCCTCCGTTAAATCCGTT 1740	81 GTTTACGGTTCGTGCTGCCTGCGTCGTCGGTTCGGCTCGGCTCGGTTCCGCCG	GlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValT
Db 3181 GCTGCTGGTCCGTTCCGAAGCTGTTCAGTGCCAACCAGGCTTTCCTGCTG Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln Db 3241 AAACTGACCCGTCACCGTGTTCCTGCTGCTGCTGCGTACCGCTCCAGG Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn Db 3301 ACCCAGCTGTCCCGTAAACTGCCGGTACCGTCTGGAAGCTGCTGCAAGCTGCTAAC Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132	3001 A7 1021 PH 3061 TT 1041 Se 3121 TC	2881 A 2881 A 2941 A	Db 2641 AAAACCTTCCTGGGTACCCTGGTTCGTGGTGTTCCGGAATACGGTTGCGTTGTTAACCTG 901 ArgLysThrValvalAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	Db 2461 CGTGGTAAATCCTACGTTCAGTGCAAGGTATCCCGCAGGTTTCCAATCCTGTCCAACCCTG Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu Db 2281 TCCCACGTTTCCACCCTGACCGACCTGCAGCCGTACAGTCGGTCAGTTCGTTGCTCACCTG Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu

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Patent No. 6617110
GENERAL INFORMATION:
                                                                                                                                                                                        TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 640:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Pc-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                             MOLECULE TYPE:
                         FEATURE:
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FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: CURNOWN>
R APPLICATION DATA:
                                                                                        LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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STATE: California
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FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                    TOPOLOGY:
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NAME/KEY:
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Percent Similarity:
Best Local Similarity:
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SEQUENCE DESCRIPTION: SEQ ID NO: 640:
 281
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                                                                                                            GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly
                                                                                                                                                                                                                                                                               GCTACTCAAGCTAGACCACCACCACATGCTTCTGGTCCAAGAAGAAGAATTGGGTTGTGAA
                                                                                                                                                                                                                                                                                                    AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu
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GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
                                                ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
                                                                                            GGTGCTGCTCCAGAACCAGAAAGAACTCCAGTTGGTCAAGGTTCTTGGGCTCATCCAGGT
                                                                                                                                                         GCTAGAAGAAGAGGTGGTTCTGCTTCTAGATCTTTGCCATTGCCAAAAAGACCAAGAAGA
                                                                                                                                                                         AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg
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                                                                                                                                                                                                                                                                                                                                            TTGGTTGCTCCATCTTGTGCTTATCAAGTTTGTGGTCCACCATTGTATCAATTGGGTGCT
                                AGAACTAGAGGTCCATCTGATAGAGGTTTTTGTGTTTCTCCCAGCTAGACCAGCTGAA
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rPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 6	rValVal 6 TGTTGTT 1	601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620 	581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600 		541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560 	521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540 	501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520 		461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProDroGlyLeuTrpGlySer 480	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460	421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440	401 AlaGlnCysBroTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400	361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360 	321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320	
do Qy	Qy Db	B 8	d d	B 84	당 왕	D Qy	Db Q	g g	Db Qy	Db Qy	db Qy	D 09	Db Qy	g dg	D Q	d dd y	B &	€ ₽
1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020 	981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000 	961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980 	941 GluvalGinSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960	GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920 	881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900 	861 GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880	841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860 	821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840 	801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820 	GlnGlı CAAGAJ	761 SerHsValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780	ValArs	721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740	701 AspProProProGiuLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720 	LeuGl TTGGG	TTGTT	GGTGCTAGAACTTTTAGAAGAGAAAAAAAAGAGCTGAAAGATTGACTTCTAGAGTTAAAGCT 1

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RESULT 9
US-09-721-456-641
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Patent No. 6617110
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R.
APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: CUNKNOWN
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California COUNTRY: USA
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SEQUENCE DESCRIPTION: SEQ ID NO: 641:
US-09-721-456-641
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Best Local Similarity:
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APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY, AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION UMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:
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                               LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla
                                                                                 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
                                                                                                                                                                                                                                                                      PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (415) 576-0300
          TIGGTIGCTCCATCTIGTGCTTACCAAGTTTGTGGTCCACCATTGTACCAATTGGGTGCT
                                                                                                                                                                 TCTTACTTGCCAAACACTGTTACTGACGCTTTGAGAGGTTCTGGTGCTTGGGGTTTGTTG
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Matches:
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181 AlaThrGinAlaNagProProProPrishalaserGlyProArgArglewGlyCyeGli 200 201 ArghlaThpashissErfalayGlinAlagClinGround (1918) 201 ArghlaThpashissErfalayGlinAlagClinGround (1918) 201 ArghlaThpashissErfalayGlinAlagClinGround (1918) 201 AlaAgCTROANCCACTCCTTNASACAAGCTCTCTTCCACTCCAAGAAGAACATCCCCCCACCACCACCACCACCACCACCACCACCAC
1621 TROCCTANGTICTROCACCONTRANCTICCOTTROCACCONTROLOGY AND ACCONTROLOGY AND

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US-09-721-456-642
US-09-721-456-642
; Sequence 642, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1121
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TLE OF INVENTION: Human Telomerase Catalytic Subunit
MBER OF SEQUENCES: 727
RRESPONDENCE ANDREWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              981
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                                                                                                                                             CITY: San Francisco
STATE: California
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                                                                                                        ZIP: 94111-3834
                                                                                                                               COUNTRY: USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGERENCY/DOCKET NUMBER: 36,429
REFERENCY/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
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FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                      ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln
    AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu
                                                                                         ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp
                                                                                                                                                 GTTTTGCCATTGGCCACCTTCGTTCGTCGTTTGGGTCCACAAGGTTGGCGTTTGGTTCAA
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                                                                                                                                                                                                                                                     MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
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Matches:
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Indels:
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421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValTh	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuP	TCCAT	21	2 2			GlyAla GGTGCC		201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 		141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValAr	81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly
nGlySerValAlaAlaProGluGlu 440 	SCYSProLeuArgAlaAlaValThr 420	uPheLeuGluLeuGlyAsnHis 400	stProGlyThrProArgArgLeuPro 380	euThrGlyAlaAro GACCGGTGCCCG	ln 34	س ص	90	84 84	yGlnGlySerTrpAlaHisProGly 260 	uProLeuProLysArgProArgArg 240		YProArgArgArgLeuGlyCysGlu 200	YProProLeuTyrGlnLeuGlyAla 180 		gGlySerGlyAlaTrpGlyLeuLeu 140	OGluAlaPheThrThrSerValArg 120	euGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100 TGCAACGTTIGTGTAACGTGGTGCCAAAAACGTTTTGGCCTTCGGT 300
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Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132	Oy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100	Qy 1041 SerLeuCysTyrSerIleLeuLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060	Oy 101 IleTyrty811eLeuLeuLeuGInAlaTyrArgEneH18AlaCy8ValLeuGInLeuPro 1020	981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1	921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 9	Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900	Oy 801 AlaSerSerGlyLeuDheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
IENGTH: 3451 base pairs TERMIDEDMESS: single TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE: NAME/KEY: - LOCATION: 13451 OTHER INFORMATION: /note= "hTRT sequence employing codon	NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 015389-002610US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0200 INFORMATION FOR SEQ ID NO: 721: SEQUENCE CLARACTERISTICS:	FILING DATE: 14-AUG-1997 PRIOR APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997 PRIOR APPLICATION NUMBER: WO PCT/US97/17885 PRIOR APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:	PRIOR APPLICATION DATA: APPLICATION UNMBER: US 08/911,312 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA: APPLICATION DATA: PRIOR APPLICATION DATA:	FILING DATE: 25-APR-1997 PRIOR APPLICATION UNMBER: US 08/851,843 FILING DATE: 06-MAY-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-WAY-1997	CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-LOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997	APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B. APPLICANT: Morin, Gregg B. APPLICANT: Harley, Calvin B. APPLICANT: Andrews, William H. TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-1884

Qy 281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300	Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280	Qy 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260	Qy 221 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProLy8ArgProArgArg 240	Qy 201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220	Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200	Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180	alLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 	Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140 	Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120	Qy 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100 	Qy 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80	Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60	QY 21 ValleuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40	Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20 	100.00% Indels: 3 Gaps: 4-692-2 (1-1132) x US-08-974-549A-721 (1-3451)	P# "	THER INFORMATION: containing SacI and XhoI sites 4-549A-721 t Scores:	OTHER INFORMATION: distribution preferentially used by OTHER INFORMATION: highly expressed genes in E. coli
Q 40	D Qy	D Qy	DB QY	용 상	db Qy	Db Qy	Qy	g 9y	g Q	D Q	g Vy	D Q	DB QY	9g 4g	Qy Db	Db Qy	문 성	DЬ
641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660 	621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640	01 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 6 	581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600 	561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580 	541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560 	521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540	501 AlaLysLeuSerLeuGlnGluLeuThrTzpLysMetSerValArgAspCysAlaTzpLeu 520	481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500 	461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460 		401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420 	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400 	361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360 	321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340 	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320	868 GAAGCTACCTCCCTGGAAGGTGCTCTGTCCGGCACCCGTCACTCCCACCCGTCCGT

	LeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSe
Db 1148 TCCTGTGCTACTICANAGCTICANAGCTGACATICCCCTGATATICCCCTGATATICCCCTGATATICCCCTGATATICCCCTGATATICCCCTGATATICCCTGATATICCCTGATATICCCTGATATICCCTGATATICCCTGATATICCCTGATATICCCTGATATICCTGA	1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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LOCATION: 1..3451

OTHER INFORMATION: /note= "hTRT sequence employing codon distribution preferentially used by highly expressed genes in E. coli containing SacI and XhoI sites"

SEQUENCE DESCRIPTION: SEQ ID NO: 721:

US-09-721-456-721
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 721:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3451 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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              LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
                                                                                                     TCCTACCTGCCGAACACCGTTACCGACGCTCTGCGTGGTTCCGGTGCTTGGGGTCTGCTG
                                                                                                                                                                        PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg
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                                                                  LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
                                                                                                                      SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
                                                                                                                                                                                                                   GTTGCTCGT
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                       ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Makamura, Toru
APPLICANT: Makamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
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ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-851-843A-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION TWORMATION:
APPLICATION NUMBER: 015389-002930US
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
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SEQUENCE CHARACTERISTICS:
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LOCATION: 56..3454
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
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821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840	801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgTle 820 	781 GlnGluThrSerProLeuArgAepAlaValValIleGluGlnSerSerSerLeuAenGlu 800 	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 	ValargargTyrAlavalValGlnLysAlaAlaHisGlyHisValargLysAlaPheLys 	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 	701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720 	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 	gValLysAla GGTGAAGGCA	LeuArgPheIleProLysProAspClyLeuArgProIleValAsnMetAspTyrValVal	601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620 	eGlyIleArgGlnHißLeuLysArgValGlnLeuArgGlu 	561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580 	541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560 	521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540 	501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520	
APPLICANT: Morin, Gregg B. APPLICANT: Harley, Calvin B. APPLICANT: Andrews, William H. TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727 CORRESPONDENCE ADDRESS:		RESULT 14 US-08-974-549A-1 ; Sequence 1, Application US/08974549A ; Patent No. 6166178	Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132	Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120	Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100	Qy 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080	Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060	Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040	Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020	Oy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000	Qy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980		Qy 921 GIMMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThKArgThrLeu 940	901 ATGLYSTINTVALVALASINENEPTOVALGIUNASIGGIUNTALEUGTYGLYYINTALAPINEVAL	881 bysinfredeunrginfleuwalargglyyalfroctulyrglycysvalvalasnieu	2636 GGGCTGCCTTGGTGGATGATTTCTTGGTGACACCTCACCCACGCG 2	2576

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Best Local
Percent Similarity:
Best Local Similarity:
                                                     Alignment Scores: Pred. No.:
                                        Score:
                                                                                                             US-08-974-549A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/915,503

PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION UNMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

PRIOR APPLICATION UNMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGINT INFORMATION:
NAME: APPLICATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

APPLICATION NUMBER: US 08/724,643

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APP.1997

PRIOR APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR.1997

PRIOR APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/911,312

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/911,312

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/911,312

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/912,951

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
BILLING DATE: 105/NVL1007
                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 14-AUG-1PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                             NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                        MOLECULE TYPE:
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CLASSIFICATION:
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STREET: Two Embarca
CITY: San Francisco
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14-AUG-1997
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/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
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Length:
Matches:
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                                                                                                                 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
                                                                                                                                                                                        GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly
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                                          CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
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641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660	1796 TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGGTGCAGGAG 1855 601 LeuSerGluAlaGluValargGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620	541 LeuAlaLysPheLeuHiSTTpLeuWetSerValTyrValValGluLeuLeuArgSerPhe 560	01 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 52	61 36 81	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 4	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 4	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
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US-08-854-050-224
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                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ADDLE: RANGOLDH T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 224, App
Patent No. 626183
                                                       TELEPHONE: (415) 576-020
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
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APPLICANT: Cech, Thomas
APPLICANT: Lingner, Joac
APPLICANT: Nakamura, Tor
                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
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                        TYPE: nucleic acid STRANDEDNESS: sing
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Best Local Similarity:
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1 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 6	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	1 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	ArgargSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520 	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 5	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 	GAGGACAGAGAGAGGATGATGATGATGATGAGGAGAGAGA	ProAlahlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 4		o μ		CysproprovalTyralaGluThrLysHispheLeuTyrSerSerGlyAspLysGluGln 340	1 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 32	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 	836 AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAA 895
Qy 981 LysCysHisSerLeuBheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000	Oy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980	941 2876	921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 94	901 2756	881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	861 2636	Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgAsp 860	821 2516	Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820	781 2396	761 2336	Qy 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaBheLys 760	721 ProGlaAspArgLeuThrGluValIIeAlaSerIleIleLysProGlaAsnThrTyrCys 7	701 AgpProPro6luLeuTyrPheValLygValAggValThrGlyAlaTyrAgpThrIle 	681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 7	Qy 661 LeuPheSerValLeuAsmTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680	641 1976	1916 CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG 1

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CTTCAAGAC	oPheLysTh	SCTCCCGG	sLeuProGl	TGTCACCTA	gValThrTy	CTCCGAGGC	SerGluAl	CCTGAAAGC	eLeuLysAl	SAAGAACCC	oLysAsnPr	CTGCAGGC	LeuGlnAl
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	ProAlaLeuProSerAspPheLysThrIleLeuAsp	ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC	ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG	LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	GCGGCCGGCCTCTGCCGTCCGAGGCCGTGCAGTGCCCACCAAGCATTCCTGCTC	AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGG	SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGC	PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValTleSerAspThrAla	ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCTGCAGCTCCCA	
AC 3451	sp 1132	rgacticcc	euThrAlaL	rccreeeer	euLeuGlyS	GCTGTGCC	pLeuCysH	CAGGGATGT	laGlyMetS	rccrecece	1eLeuArgV	TCACGCAT	ıeHisAlaC
		TGGAGGCC	euGluAla	CACTCAGG	erLeuArg	ACCAAGCA	isGlnAla 	cecreee	erLeuGly	TCATCTCT	alileSeri	GTGTGCTG	ysValLeu(
		GCAGCCAAC	AlaAlaAsr 	ACAGCCCAG	[hrAlaGlr	ricciecio	PheLeuLeu	SCCAAGGG	11aLysGly	ACACGGCC	AspThrAla	AGCTCCCA	31nLeuPro
		3415	1120	3355	1100	3295	1080	3235	1060	3175	1040	3115	1020

Search completed: October 28, 2004, 15:24:24 Job time : 432 secs

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_f/USPT0_spool/US10044692/runat_28102004_103654_1358/app_query.fasta_1.1287
-Q=/cgn2_f/USPT0_spool/US10044692/runat_28102004_103654_1358/app_query.fasta_1.1287
-DEGENEMD1 -OFWT=fastap_-SUFFIX=zge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10044692_@CGN_1_1_6972_@runat_28102004_103654_1358 -NCPU=6 -ICPU=3
-NO_MYAP_-LARGEQUERY_-NEG_SCORES=0 -WAIT_-DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use
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461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480	421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320	261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280	221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgArgLeuGlyCysGlu 200	141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
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Cech, T.R., Lingner, J., Nakamura, T., Cha Harley, C.B. and Andrews, W.H.
Cells immortalized with telomerase reve drug screening
Patent: US 6617110-A 640 09-SEP-2003;
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Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAcysLeuValCysValProTrp 60	1 MetProArgAlaProArgCy8ArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20	Score: 5961.00 Matches: 1339 Score: 5961.00 Matches: 1132 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-10-044-692-2 (1-1132) x AR393361 (1-3396)	6617110-A 641 09-SEP-2003; ocation/Qualifiers3396 organism="unknown" nol_type="genomic DNA"	Unknown. Unknown. Unclassified. Inclassified. (loases 1 to 3396) Cech, T.R., Lingner, J., Nakamura, T. Harley, C.B. and Andrews, W.H. Cells immortalized with telomerase drug screening	RESULT 4 AR393361 LOCUS AR393361 3396 bp DNA linear PAT 18-DEC-2003 DEFINITION Sequence 641 from patent US 6617110. ACCESSION AR393361 VERSION AR393361.1 GI:40118790 KEYMORDS	301 ACTCAATTGTCTAGAAAATTGCCAGGTACTACTTTGACTGCTTTGGAAGCTGCTGCTAAT 336 121 ProAlaLeuProSerAgpPheLysThrIleLeuAsp 1132 121 ProAlaLeuProSerAgpPheLysThrIleLeuAsp 1132 121 CCAGCTTTGCCATCTGATTTTAAAACTATTTTGGAT 3396	3061 TTTCATCAACAAGTTTGGAAAAATCCAACTTTTTTTTGAGAGTTATTTCTGATAC 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLy 1051 CTTTGTGTTATTTTAAAAGTGAAAGCTAAAATGCTGGTATGTTTTTGGGTGGTGTAAAATGCTGGTATGTTTTTGGATGCTAAAATGCTGGTATGTAT
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URCE Unknown. ORGANISM Unknown. Unclassified.	SOURCE ORG	<pre>821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrL</pre>
	AR393362 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	 lu 800 AA 240 820
	Oy Db RESUL1	761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
01 ThrGl	유 성	 741 ValargargTyralaValValGlnLysalaAlaHisGlyHisValargLysAlaPheLys 760
81 LysLe	g 49	721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
AlaAl GCTGC	, g . g	701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 	Ag.	PheValLeuArgValArg/ TTCGTTTTGAGAGTTAGAC
1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 	B 8	661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
IleTy	д Q	 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
981 Lyscy	D QY	621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
61 Asnar 81 AACAG	B &	 601 LeúserGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
41 GluVa 21 GAAGT	D Qy	 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 	B 8	 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSsrVal 580
901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 	р 8	541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	g dy	 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540
1 GlyLe 1 GGTTT	당 &	 rValArgAspCysAlaTrpLeu 5
841 LeucysSerLeucysTyrGlyAspMetGluAsnLysLeubheAlaGlyIleArgArgAsp 	g Q	481 ArgHisAsnGluArgArgBheLeuArgAsnThrLysLysBhsIleSerLeuGlyLysHis 500
	DЬ	 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480

Qy 261 Db 781 Qy 281 Qy 301 Db 901 Qy 321 Db 961 Db 1081 Qy 361 Db 1141 Qy 381 Db 11201 Qy 441 Db 1321 Qy 441 Db 1321 Qy 441 Db 1321 Qy 441 Db 1321 Qy 501 Db 1501 Qy 541 Db 1561 Qy 561 Db 1681 Db 1741 Qy 581 Db 1741 Qy 601

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                                                                                                               GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu
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LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn
                               AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu
                                                            GAAGTTCAATCTGATTACTCTTACGCCCGTACCTCTATTCGTGCCTCTTTGACCTTC
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Patent: WO 03095605-A 3 20-NOV-2003;
Pharmacia Italia S.p.A. (IT)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn
                                                                                                                            AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG
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KYOWA HAKKO KOGYO CO LITD,AKIHIRO UMEZAWA,JUNICHI HATA, KEI FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA
OS Homo sapiens (human)
PN WO 0148149-A/16
PD 05-UUL-2001
PF 28-FEB-2001 WO 2000JP001148
PF 28-FEB-2000 WO 2000JP001148
PF 28-FEB-2000 WO 2000JP001148
PF 28-FEB-2000 WO 2000JP001148
PR 28-BEC-1999 JP 99P 372826
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PR C12NS/06,612NS/06,612NS/06,612NS/06,612NS/06,612NS/06,612NS/06,612NS/06,61399).
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Umezawa,A., Hata,J., Fukuda,K., Satoshi, Ogawa and Sakurada,K.

Adult bone marrow-origin cell capable of differentiating into
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Adult bone marrow-origin myocardial cell.
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WO 0148149-A/16.
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
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                                                                                PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg
                                                                                                                                                              ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly
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WO 0148149-A)16
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28-DEC-1999 JP 99P 372826
AKIHIRO UNEZAWA, JUNICHI HATTA, KEIICHI FUKUDA, SATOSHI
A, KAZUHIRO SAKURADA
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Key Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
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481 ArgHisAsnGluArgAr 1441 AGGCACAACGAACGCCCG	461 ValTyrGlyPheValAr 1381 GTGTACGGCTTCGTGCG	441 GluAspThrAspProArgArg 321 GAGGACACAGACCCCCGTCGC	421 ProAlaAlaGlyValcy 1261 CCAGCAGCCGTGTCTG	401 AlaGlnCysProTyrGl 1201 GCGCAGTGCCCCTACGG	381 ArgLeuProGlnArgTy 1141 CGCCTGCCCCAGCGCTA	361 ValGluThrIlePheLe 1081 GTGGAGACCATCTTTCT	341 LeuArgProSerPheLe 1021 CTGCGGCCCTCCTTCCT	321 CysProProValTyrAl 961 TGTCCCCGGTGTACGC	301 ArgGlnHisHisAlaGl 901 CGCCAGCACCACGCGGG	281 GlualaThrSerLeuGl 841 GAAGCCACCTCTTTGGA	261 ArgThrArgGlyProSe 781 AGGACGCGTGGACCGAG	241 GlyAlaAlaProGluPr 721 GGCGCTGCCCTGAGCC	221 AlaArgArgArgGlyGl - 661 GCGAGGAGGCGCGGGGG	201 ArgAlaTrpAsnHisSe 601 CGGCCTGGAACCATAG	181 AlaThrGlnAlaArgProPi 541 GCCACTCAGGCCCGGCCCCC	161 LeuValAlaProSerCy 481 CTGGTGGCTCCCAGCTG	361 AGCTACCTGCCCAACAC 141 LeuArgArgValGlyAs 421 CTGCGCCGCGTGGGCGA
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLy 	rGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGl: 	gArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGl rcgCcTgGTgCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCA	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGl 	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAl	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAs	.ePheLeuGlySerArgProTrpMetProGlyThrProArgA 	rgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArg 	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLy 	.8HisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPr 	rSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHi 	ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgP 	ProGluProGluArgThrProValGlyGlnGlySerTrpAl 	;gGlyGlySerAlaSerArgSerLeuProLeuProLysArg) 	ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAla	oProProHisalaSerGlyProArgArgArgLeuGly 	roSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAl 	GCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTG euArgArgValG1yAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
SETLEUGlyLysHis 500 TCCCTGGGGAAGCAT 1500)GlyLeuTrpGlySer 480 	SSerSerProTrpGln 460	AlaAlaProGluGlu 440 3GCGGCCCCGAGGAG 1320	JARGAlaAlaValThr 420 3CGAGCTGCGGTCACC 1260	JLeuLeuGlyAsnHis 400 	rProArgArgLeuPro 380 rccccGcAGGTTGCCC 1140	rGlyAlaArgArgLeu 360 rGCGCTCGGAGGCTC 1080	rGlyAspLysGluGln 340 AGGCGACAAGGAGCAG 1020	ProTrpAspThrPro 320 CCCTGGGACACGCCT 960	er V)AlaArgProAlaGlu 280 GCCAGACCCGCCGAA 840	TrpAlaHisProGly 260 TGGGCCCACCCGGC 780	8—B	/LeuProAlaProGly 220 CTGCCAGCCCCGGGT 660	JArgLeuGlyCysGlu 200 CGTCTGGGATGCGAA 600	TyrGlnLeuGlyAla 180 TACCAGCTCGGCGCT 540	GCGTGGGGGCTGCTG 420 GCYBAlaLeuPheVal 160
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   Yamada,Y.

The cell having the potentiality of differentiation Patent: WO 0148150-A 16 05-JUL-2001;
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Umezawa,A., Hata,J., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. an
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PF 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001448 PI

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KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA

PC 012N5/06, C12N5/10, C12N15/09, A61K31/203, A61K35/28, A61K38/19,
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KYOWA HAKKO KOGYO CO LTD
OS Homo sapiens (human)
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PN WO 0148151-A/16
PP 27-DEC-2001
PF 27-DEC-2001 WO 2000JP009323
PR 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001 02-NOV-2000 WO PCTJP0007141
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621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640 	LeuserGluAlaGluValargGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 6	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 	PheTyrValThrGluThrFheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 58	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 56	5 4 L	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHlsSerProTrpGln 460	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380 	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360 	321 CysproprovalTyrAlaGluThrLysHispheLeuTyrSerSerGlyAspLysGluGln 340 	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320 	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 	
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000	961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 9	Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960	921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 9	Qy 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920	Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900	Qy 861 GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880	Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860	Oy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840	Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820	Qy 781 GlnGluThrSerProLeuArgAspAlaVallleGluGlnSerSerLeuAsnGlu 800	Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780		/01 ASPEROFROSTULEUTYERUSVALDYSVALABDVALLITUTYERAS (1914) 1	2041 CTGGCCTGGACGATATCCACAGGCCTGGCGCCCCAG 21	1981 CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGCCCCGGGCCTCCTGGGCGCCTCTGTG 2		1861

41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 	21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 	1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 	.414 (1-3399)	100.00% Indels: . Gaps:	Pred. No.: 6.74e-151 Length: 3399 Score: 5961.00 Matches: 1132 Scorent Similarity: 100.00% Conservative: 0 Rest Local Similarity: 100.00% Mismatches: 0	Scores:	FEATURES Location/Qualifiers 13399 /organism="Homo sapiens" /mol_type="unassigned DNA"	AUTHORS Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P. TITLE Method for inhibiting the expression of a target gene JOURNAL Patent: WO 02055693-A 28 18-JUL-2002; Ribopharma AG (DE)	4 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1		AX481414 AX481414 AX481414 AX481414 ACCUS ACCESSION Sequence 28 from Patent WO02055693. ACCESSION AX481414	1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132	1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 	1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 	1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 	1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgVallleSerAspThrAla 	1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro
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781 GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800	761 SerHisValSerThrLeuThrhepLeuGlnProTyrMetArgGlnPheValAlaHisLeu 7 	μ μ	721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740	701 AgpProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720	681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700	661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680	641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660 	621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640	601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620 	581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600 	561 PheTyrValThrgluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580 	41 21	521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540 	501 AlaLysLeuSerLeuGlmGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520 	481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500	461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460 	421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
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Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180	OY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140	81 ValalaargValLeuGlnargLeuCysGluargGlyAlaLysasnValLeuAlaPheGly	Oy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCyValProTrp 60	28 ATGCCGGTGCTCCGCGTTGCCGTGCTGTTCCCTGCTGCGTTCCCACTATCGCGAA 8 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 4	Gaps: 0 x AR393441 (1-3451) AlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 2	Alignment Scores: Pred. No.: Score: Score: Score: Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Percent Similarity: Rest Local	OURNAL PATENT: US 61/110-A /21 09-SEP-2003; FEATURES 13451 Source 13451 /organism="unknown" /mol_type="genomic DNA" ORIGIN	Unclassified. 1 (bases I to 3451) 1 (chases I to 3451) 2 (chases I to 3451) 3 (chases I to 3451) 4 (chase	LOCUS AR393441 3451 bp DNA linear PAT 18-DEC-2003 DEFINITION Sequence 721 from patent US 6617110. ACCESSION AR393441 VERSION AR393441.1 GI:40118968 KEYWORDS SOURCE Unknown. ORGANISM Unknown.
Oy 1588 CGTCGTTCTCCGGGTGTTGGTTGCGTTCCGGCTGAAACACCGTCTGCGAAAATC 1647 Db 1588 CGTCGTTCTCCGGGTGTTGGTTGCGTTCCGGCTGAACACCGTCTGCGAAAAAAACCGTCTGAACACCGTCTGAAAAAAAA	481 ATGHISASHIGIUATGATGPHELEUATGASHITITLYSBLYSBFIGLIESETLEUGIYLYSBIIB	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	1228 421 1288	Oy 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400	TIGABAACTATCTTCCTGGGTTCCCGTCCGTCGGTCGGCGCGCGC	321 988	Oy 281 SUMAGINESELEGIC USTANDAMENSEL STATEMENT STATEMENT OF THE STATEMENT	748 GGTGCTGCTCCGGAACCGGAACCGGACCCCGGTTGGTCAGGGTTCCTGGGCTCACCCGGGT 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg

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GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe
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Location/Qualifiers
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Cech, T.R. and Lingner, J.
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MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu
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Cech,T.R. and Nakamura,T.
Telomerase
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Patent: JP 2002509716-A 1 02-APR-2002;
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OS Homo sapiens (human)
PN JP 2002509716-A/1
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541280
PF 31-MAR-1998 US 60/112006
PR 31-MAR-1998 US 60/112006
PR 31-MAR-1998 US 67/112006
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PC C12N15/09,C12N5/00,A61K37/48,C12N5/00,C12N15/00 CC telomerase reverse transcriptase (hTRT) FH Key Location/Qualifiers
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/mol_type="genomic DNA"
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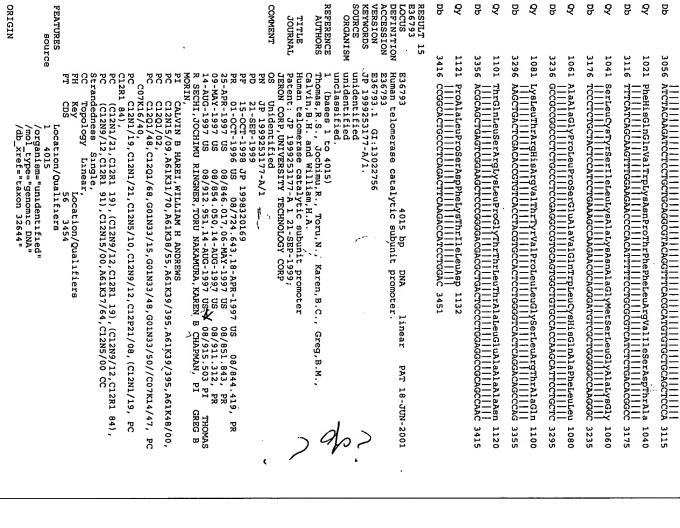
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Percent Similarity:
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DB: 음 성 음 성 S S 밁 밁 밁 ঠ 밁 S US-10-044-692-2 (1-1132) x E36793 (1-4015) Pred. No.: Alignment Scores: 176 116 41 61 21 56 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp GTGCTGCCGCTGGCCACGTTCGTGCGGCCCCTGGGGGCCCCCAGGGCTGGCGGCTGGTGCAG ATGCCGCGCGCCCCCCGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 7.86e-151 5961.00 100.00% 100.00% Length: Matches: Conservative: Gaps: Mismatches: Indels: 4015 1132 0 0 60 80 40 115 20 295 175

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rMetArgGlnPheValAlaHisLeu |||||||||||||| |TGCGACAGTTCGTGGCTCACCTG 2395 nSerSerSerLeuAsnGlu AlaValArgIle 2515

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TCCTGCTC 3295	GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3295	3236	οь
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Search completed: October 28, 2004, 12:50:01 Job time : 11572 secs

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ALIGNMENTS

γ	B &	D QQ	g 8	g V	Query Match Best Local Si Matches 4015;	RESULT 1 ARIJ04587 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORGIN
241 ACGGCCGCCCCCCCCCCCCCCCCCCCCAGGTGTCCCTGCCTG	181 GGACCCGGCGGCTTTCCGCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCCCTGGGACGC 240	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180	61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120	1 GCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60	Match 100.0%; Score 4015; DB 6; Length 4015; Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; es 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AR104587 AR104587 AR104587 AR104587 AR104587 AR104587.1 GI:12817295 . Unknown. Unclassified. 1 (bases 1 to 4015) Cech,T.R. and Lingner,J. Telomerase Patent: US 6093809-A 224 25-JUL-2000; Location/Qualifiers 1. 4015 /organism="unknown" /mol_type="unassigned DNA"

2401 GACCAGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460 2401 GACCAGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460		9 1321 AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGGCCGCCCCGAGGAGGAAGA 138 	, o
CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGGTTCGTGGCTCACCTGCAGGA		y 1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACCCCAGC 1320	40 40
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981 CAGAACGTTCCGCAGAGAAAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT		y 901 CACCTCTTTGGAGGTGCGCTCTCTGGCACGCCACTCCATCCGTGGGCCGCCA 960	45 45
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 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGCCCACAGCCAGGCCAGGCCGA
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                                                 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC
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181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGCGTGC	61 GCGCTCCCCGCTGCCGAACCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAAGTGCT 120	100.0%; Score 4015; DB 6; Length 4015; al Similarity 100.0%; Pred. No. 0; 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGATGCC 60 1	AR175848 AR175848 Sequence 224 from patent US 6309867. AR175848.1 AR175848.1 GI:17917147 Unknown. Unclassified. 1 (bases 1 to 4015) Cech, T.R. and Nakamura, T. Telomerase Patent: US 6309867-A 224 30-OCT-2001; Location/Qualifiers 1. 4015 /organism="unknown" /mol_type="unassigned DNA"	

1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA 1380	GTGCCCCTACGGGTGCTCCTCAAGACGCACTGCCCCTGCGAGCTGCGGTCACCCCAGC		GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCCTTGCCCCGCAGGTTGCCCCGCCCTTGCCCCGCAGGTTGCCCCGCCCTTGCCCCGCAGGTTGCCCCGCCCTTGCCCCGCAGGTTGCCCCGCCCTTGCACCATGCCCAGGATGCCAAGGACTCCCCCGCAGGTTGCCCCGCCCTTGCAGGACTCCCCCGAGGTTGCCCCGCCCTTGCACGCCTTGCCCCGCAGGTTGCCCCGCCCTTGCACGGACTCCCCCGAGGTTGCCCCGCCCTTGCACGCTTGCCCCGCAGGTTGCCCCGCCCTTGCACGCTTGCCCCGCCCTTGCACGCTTGCCCCGCCTTGCACGCTTGCCCCGCAGGTTGCCCCCCCC	GCCCTCCTTACTCAGCTCTGAGGCCCAGCCTGACTGGCGCTCGAGCTCGTGGA	CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG	GCACCACGCGGGCCCCCATCCACATCGACACGCCACCTCCTCGGGACACGCCTTGTCC	CACCTCTTTGGAGGGTGCGCTCTTGGCACGCGCCACTCCCACCCA	GCTTGGACCGAGTGACCGTGGTTTCTGTGTGTGTGTCACCTGCCAGACCGCCGAAGAAGC	781 TGCCCCTGAGCCGGAGCGGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGGCAGTGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC 780	CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG	601 TCAGGCCCGGCCACCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCAC 600	481 CCGCGTGGGCACGACGTGCTGGTTCACCTGCTGCACGCTGCGCGCTCTTTGTGCTGGT 540	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGGGGG	361 GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCGAGCGTGCGCAGCTA 420	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360	241 ACGGCCGCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCCTG
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PF 30-MAR-1999 JP 2000541280
PR 31-MAR-1998 US 60/112006
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PC C12N5/06,A61K35/14,A61K38/43,A61K39
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 4015)
Gaeta, F.C.A.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                              C12N5/10,
PC C12N15/09,C12N5/00,A61K37/48,C12N5/00,C12N15/00
telomerase reverse transcriptase (hTRT) FH Key
                                                                                                                                                                                                                                                                                                                                                                                            BD218834.1 GI:33028604
JP 2002509716-A/1.
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Method and composition
                                                                                                                       Location/Qualifiers FT CDS
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                                                                                                                                                                                                                                                                                                           Method and composition for inducing immune
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31-MAR-1998 US 60/112006
FEDERICO CA GABTA
C12N5/06,A61K35/14,A61K38/43,A61K39/00,A61P35/00,A61P37/00,
                                                                                                        (56). (3454).
Location/Qualifiers
                                                           /organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                               .4015
 Score 4015;
Pred. No. 0;
0; Mismatches
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901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	721 GAGGCGCGGGGGAGTGCCAAGCCGAAGTCTGCCCAAAGAGGCCCAAGACCGAAGACGCCCAAGACCGAAGACCGAAGACCCCAAGACCCAAGACCCCAAGACCCCAAGACCCCAAGACCCCAAGACCCCAAGACCCCAAGACCCAAGACCAACCCAAGACCAACCCAAGACCAACCCAAGACCCAACCCAAGACCCAACCCAAGAACCCAACCCAAACCAACCCAAACCAACCCAAAGAAACCCAAGAACCCAAGAAACCAAGAAACCCAAGAACCCAAAGAAAACCCAAGAACCCAAAAGAAAACCCAACCAAAAAA	601 TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660	81 CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTTGTGCTGGT 5	301 CCGAGTGCTGCAGAGGCTGTGCGAGGCGCGGAGAACAACGTGCTGGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTTCGCCTACACACGTGCGCAGCCTACACACGCTACACACGTGACCAGCGAGCCCCCCCGAGGCCTTCACCACCACCACCAGCGTACACGCTACACGCGGGGCCCCCCCC	181 GGACCCGGCGGCTTTCCGCGCGCGTGGTGGCCCAGTGCCTGGTGTGCGTGC	1 GCAGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCCGGCAATGCC 60
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Q	o ob	0 Db Qy Db	0 2 2 2 2	D	2 2 2 2 3	Q
1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTTCCACCTCGAGGGTGAAGGCACTGTT 2040 1981 CAGAACGTTCCGCAGAGAAAAGAGGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040 2041 CAGCGTGCTCAACTACGAGGAGAAAAGAGGGCCCGAGCGTCTCCTGGGCGCCTCTGTGCTGGG 2100	GGAA GGAA CTTC		1561 GCTCTGCTGCAGGAGCTGAACGTGGAAGATGAGCGTGCGGACTGCCCTTGGCTTGGCTGCAGAG 1620	1481 CACAGACCCCCGTCGCCTGCAGCAGCCCCCAGCACACAGCAGCCCCAGGCACAGCCAGCACAGCCAGCCCCAGGCCTCCAGGCCAAGCCAGCC	### CACAGACCCCCGTCGCCGGGGAGAAGCCCCCAGGCACGCAC	1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGAGGCTCGTGGA 1140

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5. Jochimu,R., Toru,N., Karen,B.C., Greg,B.
6. H. and William,H.A.
10 compared catalytic subunit promoter
10 p 199253177-A 1 21-SEP-1999;
11 p 199253177-TBCHNOLOGY CORP
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3177-A/1.
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OS Unidentified PN JP 1999253177-A/1 PD 21-SEP-199 PT 15-OCT-1998 JP 1998320169 PR 01-OCT-1996 US 08/724.643,18-AM 25-APR-1997 US 08/846 017,06-MAY-1

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Best Local Similarity
Matches 4015; Conserv
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14-AUG-1997 US
R SECHI, JOCHIMU
MORIN,
PI CALVIN B HJ
PC C12N15/09,
PC C12Q1/02,
PC C12Q1/48, C1
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PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 56 .3454.
                                                 TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC
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C C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19,
      CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCCGGGTGCGAG
                              TCAGGCCCGGCCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC
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                                                                                                         GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC
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4-AUG-1997 US 08/912.951,14-AUG-1997 US (
SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B
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C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
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C12X15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
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Location/Qualifiers
1. .4015
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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100.0%; F
htive 0;
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B CHAPMAN, PI
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601 TCAGGCCCGGCCCCCCCCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 6	541 541		Qy 421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGGGGG	Qy 361 GCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420	Qy 301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGC 360	Qy 241 ACGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Qy 181 GGACCCGGCGCGCTTTCCGCGCGCTGGTGGCCCAGTGCCTTGGTGTGCCTTGGGACGC 240	OY 121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180	OY 61 GCGCGCTCCCCGCTGCCGAGCCGTGCCGCTGCTGCTGCAGCCACTACCGCGAGGTGCT 120	GGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60	Query Match 100.0%; Score 4015; DB 6; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ource 1.4015 /organism="unknown" /mol_type="genomic DNA"	for the t	4015)	AR224455 AR224455.1 GI:23333293 Unknown.	RESULT 6 AR224455 AR224455 LOCUS AR224455 DEFINITION Sequence 1 from patent US 6440735.	3961 GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA	OV 3961 GAGGTGCTCTCGGGAGTAAAATACTGGAATTATGACTTTTTTCACTTTTTCACTTTTTTCACTTTTTTCACTTTTTT	Mon Nov 1 10:45:58 2004 us-10-044-692-
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AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN Query Mat Best Loca Matches 4 Qy Db Db 1	Qy 39 Qy 39 Db 39 RESULT 7 AR226390 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE
Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Antrews, H.H. B Antisense compositions for detecting and inhibiting telomerase reverse transcriptase NL Patent: US 6444650-A 1 03-SER-2002; Localishiarity 100.0%; Score 4015; DB 6; Length 4015; Localishiarity 100.0%; Score 4015; DB 6; Length 4015; Localishiarity 100.0%; Pred. No. 0; Localishialrity 100.0%; Pred. No. 0; Localishialr	
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301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGGGGGGAGAAACGTGCTTGGCTTCGGCTTTCGC 360	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GCAGCGCTGCGTCCTGCTGCGCCACCTGGGAAGCCCTGGCCACCCCCGGATGCC 60	AR263555 GI:28075300 AR263555 SOURCE ORGANISM Unclassified. Unclassified. 1 (bases 1 to 4015) AUTHORS AUT	3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
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Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.
Harley,C.B. and Andrews,W.H.
Antisense compositions for detecting and inhibiting telome reverse transcriptase
Patent: US 6627619-A 1 30-SEP-2003;
Location/Qualifiers
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181 GBACCCGGCGGCTTTCCGCCGCTGGTCGCCTGGTGGCGTGCCCTGGGACGC 240		1 GCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCACCCCGGGATGCC 60 1 GCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCGATGCC 60 1 GCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCACCCCCGGGATGCC 60 1 GCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCACCCCCGGGATGCC 60	/organism="unknown" /mol_type="genomic DNA" 100.0%; Score 4015; DB 6; Length 4015; illarity 100.0%; Pred. No. 0;	1 (Chan Quan Pate		AR438403 4015 bp DNA linear PAT 20-FEB-2004 N Sequence 1 from patent US 6664046. AR438403 5R438403.1 GI:42663256	3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015		3900	3781 CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTTGCCTTCCACCCCACCCA	3780	661 GAGTGTCCAGCACCCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720
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1261 GTGCCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTCCAGGCACCCCAGGCTCCTACGGGTGCCCTACGGGTGCCCCTACGGGTGCCCCCGGAGAGACCCCCAGGCACTGCCGCCCCGAGGAGAGAGA	1141 GACCATCITICTGGGITCCAGGCCCTGGATGCCAGGACTCCCCCAGGITGCCAGGTTGCCAGGCTACTGGGAACTCCCCCAGGCAGGTTGCCACGCCAGGCCAGTTTCTGGAACCTGCTTTGGGAACCACGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCAGAGCAG	1081 GCCCTCCTTCCTACTCAGCTCTGAGGCCCAGCCTGACTGGCGCTCGAGGCTCGTGAGGCTCGTGAGGCCTGACTGGCGCTCGAGGCTCGTGAGGCCTGACTGGCGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCTCGAGGCCTGACTGCCCCGCAGGTTCGCCCCGCCT	961 GCACCACGACGCCGCCCCCCATCCACACCTCCCTCAGGACACGCCCTCGCCCCCCCC	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCCACTCCCATCCGTGGGCCGCCA 960	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGGTGTCACCTGCCAGACCCGCCGAAGAAGC 900	721 GAGGGGGGGGGGGGGGGGCGAGGCGAAGTCLGCCGLTGCCCAAAAGTCLAAAGTCLAAAGTCLAAAGTCLGCGGGCAAGGACCCGGGGAAGGACCCGGGGAAGGACCCGGGCAAGGACCCGGGCAAGGACCCGGGCAAGGACCCGGGCAAGGACCCGTTGGGCAGGGGTCCTTGGGCCCACCCGGGCAAGGACCCGTTGGGCAGGGGTCCTTGGGCCCACCCGGGCAGGACCCGGAGCAGGACCCGGTTGGGCAGGGGTCCTTGGGCCCACCCGGGCAGGACCCAACCCGGGCAAGGACCAAGGACCAAGGACCAACCCGGGCAAGAGACAAGAAG	. 12	601 TCAGGACCCCACCCCACCCCACGCCACACACCCAAAGGCCGACCCAAAGGCCGCC	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTGCGCGCTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAACGGCGCTGCCAACGGCGCTGCGAACGGGGTCTGGGATGCGAACGGGGCTCTGGGATGCGAACGGGGCTCTGGGATGCGAACGGGGCTCTGGGATGCGAACGGGGCTCTGGGATGCGAACGGGGCTCTGGGATGCGAACGGGGCTAGTGGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGGGGCTAGTGAACGAGACTAGAACAGAGAACAACAACAACAACAACAACAACAACAACA	481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCTCTTTGTGCTGGT	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGGGTGGGGGCTGCTGCTGCG 	361 GCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420

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2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520	2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460	2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCCGCGTACGACACCATCCCCCA 2220	2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC 2160	2041 CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGGCCTCTGTGCCTGGG 2100	1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGGGTCTCACCTCGAGGGTGAAGGCACTGTT 2040	1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860	1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800	1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTCTT	1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	1561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTGGCTGCGCAG 1620	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560 		381 CACAGACCCCCGTCGCCTGGTGCAGCTGCTGCCCCAGCACAGCAGCCCCTGGCA
₽ .	S B 7	S & S	P &	S B &	S B 8	, B &) B 4	S B &	S B &	S B &	?	S B 7	Q B 4	?	S B .	g B :	8 8	δ
		3421 ACTOCCTICAGACTICAGACCATCCTGGACTGACGTCCTAGGGGAGGGG			3241 GGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATICCTGCTCAAGCT 3241 CGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3241 CGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3241 CGGCCCTCTGCACACGCCTTAAGCTGCCACTGATGCCACCAAGCATTCCTGCTCAAGCT 3261 GACTTCAACACCACTCAAGCTTGACGCTTAACTCAAGACAAGCATTCAAGCATAAGCATAAGCATAAGCATAAGCATAAGCATAAGACAAGAAAAAA	CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGGCCAAGGGCGCGC 		CAAGATUCITUTUGA BORAGOCO ACASTITUTUCACORTOS TOTOCAGOROS CONCOCORTUTUCA CAAGATUCITUTUGA BORAGOCO CATUTUCA CAAGATUCTUCO COCOCOCOCOCO COCOCOCOCOCOCOCOCOCOCOC	TCACAGCTIGIIICTGAATTTTGCAGGTGAACAGCCTCCAGACGTGCAGCTCCATTTTCACAGAGCCTGCTATCTCACATCTA	CGGCTTCAAGGCTGCGGAACATCGCGCAAACTCTTTGGGGTCTTGCACCAACATCTA	CCACATACATACATCAGAGGA A CATAGAGGTCGGA A A A CTICTTTGGGGGTTGTGAGGTTGAAGTG	CLOGGERATE TO THE CONTROL OF THE CON	GCCGGCCACGGCCTATTCCCCTGTAGAAGACGACGCTGCTGGATACCCGGGACCCTGGAGGGT				2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGGTCCATCCTCCACGCTGCTCTG 2580 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTTGCGGGGGATTCCGCGGGACGGGCT 2640	2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCTG 2580

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¥	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT 3660
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¥	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCCGGCTCCACCCCA 3720
ъ	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720
У	3721	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCCACATAGGAATAGTCCATCC 3780
9	3721	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
γ	3781	CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTCCTT
ğ	3781	CAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTTTGCCTTCCACCCCCACCATCC 3840
ΣY	3841	AGGTGGAGACCCTGAGAAGGACCCCTGGGAACTTTGGGAATTTTGGAGTGACCAAAGGTGTG 3900
B	3841	AGGTGGAGACCCTGAGAACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
Ŋ	3901	CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
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δ	3961	GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015
용	3961	GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
Search co	omple: 16	Search completed: October 29, 2004, 20:54:42 Job time : 16400 secs

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-QC/cgn2 1/USPTO_spool/US10044692/runat 28102004 103655 1370/app_query.fasta_1.1287
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -WAIRIX-blosum62 -TRANS-bluman40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044692_GCGN 1 1_4804 @runat 28102004 103655_1370 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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AY407349 Homo sapi
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BM453198 AGENCOURT
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BM824748 K-EST0096
BQ258274 NISC kp11
CR688161 Tetraodon
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ALIGNMENTS

RESULT 1

FEATURES source	COMMENT	TITLE		AUTHORS	PUBMED	JOURNAL	TITLE				ARTHORS			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AY407349
them based on alignment. Location/Qualifiers 11826	Submitted (15-NOV-2003) Reterd Genomics, 43 west Gude Dilve, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering	Adams, M.D. and Cargill, M. Adams, M.D. and Cargill, M. Direct Submission Color Color As Wort Code Drive	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,	14671302	gene crios Science 302 (5652), 1960-1963 (2003)	Inferring nonneutral evolution from human-chimp-mouse orthologous	Adams, M.D. and Cargill, M.	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	Clark A.G. Glanowski S. Nielson R. Thomas P. Kejariwal A.,	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	GSS.	AY407349.1' GI:39763320	ĀY407349	genomic survey sequence.	iens TERT gene, VIRTUAL TRANSCRIPT,	AY407349 1826 bp DNA linear GSS 15-DEC-2003	

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Best Local Similarity:
Query Match:
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                                       TTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCG
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/gene="TERT"
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AY407350 1584 bp DNA linear GSS 15-DEC-2003 Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence,

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
Submitted (16.NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20080, USA
This sequence was made by sequencing genomic exons and orderin them based on alignment.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 1584)
Nielson.R., Thomas, P., Ke
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Science 302 (5652), 1960-1963 (2003)
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ArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeu
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                                            AAGCCTGACGGGCTGCGGCCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTC
                                                           LysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPhe
                                                                                               GTCAGGCAGCATCAGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
|mol_type="genomic DNA"
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132 CAGAAGAACAGGCTCTTCTACCGTAAGAGTGTGTGGAGCAAGCTGCAGAGCATTGGA 191 589 IleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGluValArgGln 608	GlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGly	MetSerValTyrValValGluLeuLeuArgSerphePheTyrValThrGluThrThrPhe	529 ValProAlaAlaGluHisArgL	30.28% Indels: 9 Gaps: 9 AV407751 (1-1835)	Pred, NO.: 1.17e-114 Length: 1835 Score: 1805.00 Matches: 373 Secoret Similarity: 69.56% Conservative: 52 Rest Local Similarity: 61.05% Mismarches: 176 Rest Local Similarity: 61.05% Mismarches: 176	/locus_tag="HCM2861"	/db xryper yenunc pan /db xryper = 10090" /db xryper = 10090" /10. >1835		them based on alignment. Location/Qualifiers	Direct Submission Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA This secuence was made by secuencing den	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Carqill, M.	14671302 (2002/, 1300-1303 (2003) 2 (bases 1 to 1835)	gene trios Gene trios Gene trios Gene trios Gene trios	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1835) Clark a.G. Glancuski G. Nielson B. Thomas B. Veiarival A.	GSS. Mus musculus (house mouse) Mus musculus	AY407315 Date of Description AY407315 AY407311 GI:39763322	Q Z Þ	1563 ATCCTGAAAGCCAAGAACGCA 1583	1046 IleLeuLysAlaLysAsnAla 1052		1026 TrpLysAsnProThrPhePheLeuArgVallleSerAspThrAlaSerLeuCysTyrSer 1045
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RESULT 4
BM453198
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                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12208 row: p column: 01
High quality sequence stop: 646.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 925)
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AGENCOURT 6387556 NIH MGC_71
5', mRNA sequence.
BM453198
                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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/lab_host="DH10B (phage-resistant)"
                                            /organism="Homo sapiens"
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                                                  ThrPheAsnArgGlyPheLysAla--GlyArgAsnMetArgArgLys 973
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                                ACCTTCAACCGCGGCTTCAAAGGCTGGGAAGGAACATGCGTCGCAAA
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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851 bp mRNA linear EST 15-JUL-
UI-M-FI0-byx-f-12-0-UI.rl NIH_BMAP_FI0 Mus musculus cDNA clone
IMAGE:6400523 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin,
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/clone="IMAGE:6400523"
/tissue_type="whole brain"
/dev_stage="mbryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP F10"
/clone li
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EST.
Mus musculus (house moundus musculus
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 851)
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BG917907
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AGCATCTGCAGGATTCAGATGCCAGTGCACTGAGGAACTCCGTTGTCATCGAGCAGAGAC
                                                                                 Contact: Robert Strausberg,
                                                                                                    Unpublished (1999)
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Sciurognathi; Muridae; Murinae; Mus
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                    IleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSer 1055
                                                                                                                                                  ThrValCysThrAsnIleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCys 1015
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/sex="female, virgin"
/tissue_type="infiltrating
/dev stage="5 months"
/lab_host="DH10B"
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/mol_type="mRNA"
/strain="FVB/N"
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Xim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sceun-dong Yuseng-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
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           /clone lib="$22$NU16n1"
/note="forgan: Stomach; Vector: pTTT3-Pac; Site_1: EcoRI;
Site_2: NotI; The $22$NU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-15 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                       cell_type="Lymphoblast-like"
cell_line="SNU-16"
                                                                                                                                                                                                                                                                                                                     tissue_type="Ascites"
                                                                                                                                                                                                                                                                                                                                                                     .one="S22SNU16n1-99-E07"
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Percent Similarity: Best Local Similarity:

5.07e-44 776.00 100.00% 100.00% 13.02%

Length:
Matches:
Conservative:
Mismatches:

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Score:

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NISC kp11904.q3 Baker mouse embryo
IMAGE:5409222, mRNA sequence
BQ258274
                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: J. Baker (Stanford University)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
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BQ258274.1 GI:20459030
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1 (bases 1 to 664)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/organism="Mus musculus"
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/strain="CD-1"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/tissue_type="embryo, late g:
                                                                                                                                                                                                       Location/Qualifiers
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RESULT 9 CR688161

LOCUS DEFINITION

> CR688161 Tetraodon

1424 bp nigroviridis full-length

mRNA cDNA

linear

HTC 12-AUG-2004

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                               ATGTGGAAGATGAAAGTAGAGGATTGCCACTGGCTCCGCAGCAGCCAGGGAAAGGACCGT
                                                                                                                                                                   ThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArgSerProGlyValGlyCys
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 CAGAAGAACAGGCTCTTCTTACCGTAAGAGTGTGTGGAGCAAGCTG
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/clone lib="Baker mouse embryo e7.5"
/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
/note="Vector: pCS105; Site 1: NotI; Site 0: Adaptor:
SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCACCGCGTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."
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/lab_host="XL1-Blue"
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72.03%
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Matches:
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Indels:
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CR688161.1
HTC; cDNA;
Tetraodon
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail: seqrefogenoscope.cns.fr - Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes; Tetradontoidea; Tetradontidae.
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ThrPheAsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeu
                                                                                                 PheValGlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArg
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                            AATCTCGACATCTATAAAGACTATTCTAGCTATGCAAACCTGTCCTTGCGCTACAGCCTT
                                                  ThrLeuGluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu
                                                                              AATCCTCAGAAGATTGTGGTCAATTTTGAGGATTCTGAGAGCACAAACTCTTGTCCTGGC
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/db_xref="taxon:47144"
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                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                             (BMAP)
                                                                                                                                               primer: pYX-5
                                                     clone="IMAGE:30355746"
                                                                              mol_type="mRNA"
strain="C57BL/6"
                                                                                                        organism="Mus musculus"
                                                                                                                                 ocation/Qualifiers
                                                                                                                       .649
                                                                  _xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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561 ACTTTAGGCCCCTGCCACTGTGCTGGACAGCAATGAAGAGAAAACTGAT-GGC---TTC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 649)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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UI-M-FY0-cgp-c-19-0-UI.rl NIH_BMAP_FY0 Mus
IMAGE:30355746 5', mRNA sequence.
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/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
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                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACACA. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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UI-M-FYO-cgp-m-21-0-UI.rl NIH_BMAP_FYO Mus
IMAGE:30355988 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                       /tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH108 (T1 phage resistant)"
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/clone lib="NIH BMAP_FYO"
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/note "Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note "Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note "Organ: p
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                                                                                                                                                                                                                                                                                    /strain="C57BL/6"
/db_xref="taxon:10090"
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   primed with oligo-dT
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gThrProValGlyGlnGlySerTrp-AlaHisProGl 260	41 GlyAlaAlaProGluProGluArgThrProValGl	0у 2
582	582	Db 5
aSerArgSerLeuProLeuProLysArgProArgArg 240	21 AlaArgArgArgGlyGlySerAlaSerArgS	Qy 2
582	82	Db 5
SerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220	01 ArgAlaTrpAsnHis	0у 2
582	82	Db 5
oHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200	81 AlaThrGlnAlaArgProProProHisAlaS	0γ 1
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180	59	Qy 1 Db 5
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4 4	39	- 42
:::	79	
yGlyGlyProProGluAlaPheThrThrSerValArg 120	01	Qy 1
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100 :::	81 19	Db Qy
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80	59 59	Qy Db 2
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60 - 	41 99	Qy 1
ValleuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40 	21 ValieuProLeuAlaThrPheValArgArgLeuGl 	Qy Db 1
MetFroArgAlaProArgCyBArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20 	1 Met ProArgâlaProArgCyBArgAlaValArgSe 	dg Qy
L-688)	92-2 (1-1132) x CF531121 (1-6	US-10-044-6
Length: 688 Matches: 154 Conservative: 17 Mismatches: 32 Indels: 166 Gaps: 2	3.45e-36 Length: 666.50 Matches: 46.34% Conservat 9: 41.73% Mismatch 11.18% Indels: 7 Gaps:	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit Query Match: DB:
primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	primer containing a Not I si size selected according to m with EcoR I adaptor, digeste directionally into pyx-Asc v sequence located between the is AGCGACACAG. This library Iowa Brain Anatomy Project (Developing Mouse Nervous Sys Institute of Mental Health (program coordinator."	ORIGIN

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	constructed by Bento Soares and M. Fatima Bonaldo."	and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was	J. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I	primed with a Not I - oligo(dT) primer [5TGTTACCAACTGAAGTGAGAGGCGGCTCATTTTTTTTTT	provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER), cDNA synthesis was	was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IqD-).	, ,0,1	t	/Clone="Recominal Center R Cell" /tiesus type="Germinal Center R Cell"	/LYPALLENIE INVIKO BODITELIO /MOL TYPOE "MENUA" /AD VIOLE "ILIVOR", BEDECT	1. 389 1. 389	High quality sequence eve at the macranam thigh quality sequence stop: 385.	Insert Length: 2187 Std Error: 0.00	This clone is available royalty-free through LLNL; contact the	unpublished (1997) Contact: Robert Strausberg, Ph.D. Email. Coaphe-romail rib COV	Index	NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Passes Traditute Cancer Garome bratomy Project (CGAD)		ns (human) ns	AA281296.1 GI:1924194 EST.	ice	AA281296 389 bp mRNA linear EST 14-AUG-1997 zt08g02.rl NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:712562 5',	64 GGTGGAGATCATCTTTCTGGGCTCA 688	360 uValGluThrIlePheLeuGlySer 368	604 TCTAAACCCCTCATTCCTACTCAGCANCCTCCAGCCTAACTTGACTGGGGCCAGGAGACT 663	340 nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe 360	599GAGCG 603	320 oCysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGl 340	598 598	300 yArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPr 320	598 598	280 uGluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGl 300	98 598	260 yArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGl 280

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1 (bases 1 to 599)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Sogabe, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730412M20 5', mRNA sequence.
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (house mouse)
                                                                                                                     81-45-503-9216
                                                                               genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
ci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                       21 ValleuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln
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                                                                                                                                                                                                                                                                   1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                           ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp
{\tt AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu}
                                                /clone lib="RIKKN full-length enriched, 8 days embryo" /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
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/lab_host="DH10B"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,
Lebkowski,J and Stanton,L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 409)
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Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 409 Std Error:
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from undifferentiated hES cell lines H1 (p22), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/mbl_type="mrNa)
/db xref="taxon:9606"
/tiBsue_type="embryonic stem cells, cell lines H1,
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BE371943.1
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DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM8748 row: h column: 07

High quality sequence stop: 639.

Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE371943 866 bp mRNA linear EST 21-JUL-2000 601217728F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/strain="CZECH II"
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945 AspTyrSerSerTyrAlaArg 951
                                                                                                                              905 ValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAla 924
                                                                                                            64 TATACGCAGTGCCAGGCATCCCCCAAGGCTCCAGCCTATCCACCCTGCTCTGCAGTCTG 123
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Search completed: October 28, 2004, 15:17:31 Job time : 7866 secs

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Run

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 _1/USPTO_spool/US10044692/runat_28102004_113043_5483/app_query.fasta_1.1287
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HeapsIZE=500 -MINILEN=0 -MAXIEN=200000000
-USER=US10044692_@CGN 1 1_4804_@runat_28102004_113043_5483 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WARIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -TMEDUT=30 -THREADS=1 -XGAPEPST=0.5 -FGAPOP=6
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1 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                             2 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.
                                                                                                                                         gene trios
Science 302 (5652), 1960-1963 (2003)
         This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                        Direct Submission
Submitted (16-NOV-2003) Celera
                                                                                                                                                                                                                                                                                                                 genomic survey sequence AY407349
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Query DB:

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Percent Similarity:
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Query Match:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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646 ArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeu 665	626 LYSProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPhe 645	606 ValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIlePro 625	586 SerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGlu 605 	566 ThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGln 585	546 HisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGlu 565 	526 ValGlyCysValF	36.37% Indels: 9 Gaps:	nment Scores: . No.: 5.54e-140 Length: 1584 e: 2168.00 Matches: 432 ent Similarity: 82.73% Conservative: 4 Local Similarity: 81.97% Mismatches: 91	/locus_tag="HCM2861"	/db_xref="taxon:9598" <1>1584 /reno="TERF"		them based on alignment. Location/Qualifiers	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	Schence 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 1584)	nneutral evolution	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. 1 (bases 1 to 1584) Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,	Pan troglodytes (chimpanzee) Pan troglodytes Pan troglodytes Pan troglodytes	AY407350.1 GI:39763321 GSS.	genomic survey sequence.
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OY 529 ValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTrpLeu 548	Alignment Scores: Pred. No.: 1.17e-114 Score: 1805.00 Percent Similarity: 69.56\$ Best Local Similarity: 61.05\$ Guery Match: 30.28\$ Conservative: 176 Mismatches: 176 DB: Gaps: 3	/or /mc /dr <1. /1c	TITLE Direct Submitselon (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers SOURCE 1.1835	JOURNAL Science 302 (5652), 1960-1963 (2003) PUBMED 14671302 REFERENCE 2 (bases 1 to 1835) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; R. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; N CE 1 (bases 1 to 1835) RS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejan Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murph, Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, Adams, M.D. and Cargill, M.	AY407351 Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial genomic survey sequence. N AY407351 AY407351 AY407351.1 GI:39763322 GSS. Mus musculus (house mouse) Mus musculus	Qy 1026 TrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyrSer 1045 :::
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 925)

NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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AGENCOURT 6387556 NIH MGC_71
5', mRNA Bequence.
BM45.1198
                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                http://image.llnl.gov
Plate: LLAM12208 row: p column:
High quality sequence stop: 646.
Location/Qualifiers
                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Matches:
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/clone_lib="NIH_MGC_71"
/clone="Organ: uTerus; Vector: pCMV-SPORT6; Site_1: Not
/note="Organ: uTerus; Vector: pCMV-SPORT6; Site_1: Not
/site_2: Sall; cloned unidirectionally. Primer: Oligo
Average insert size 2.1 kb. " NotI;

								•								
Db 78:	Оу 95	Qy 93 Db 72	Qy 91:	Qy 89	Qy 879 Db 543	Qy 859 Db 489	Qy 839 Db 423	Qy 819 Db 363	Qy 799 Db 301	Qy 779 Db 241	Qy 759 Db 183	Qy 739 Db 12	Qy 719	Qy 699 Db 3	US-10-044-692	Alignment Sco Pred. No.: Score: Percent Simil Best Local Si- Query Match: DB:
3 ACCTTCAACCGCGGCTTC	9 ThrPheAsnArgGlyPheLysAlaGlyArgAsnMetArg	99 ThrLeuGluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu 958 	19 PheValGlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArg 938 	9 AsnLeuArgLysThrValValAsnPhePro 	9 HisAlaLysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValVal 898	39 ArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThr 878 	9 ThrLeuLeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArg 858 	3 ArglleArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSer 838	99 AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaVal 818 	9 HisLeuGlnGluThrSerProLeuArgAspAlaVallVallleGluGlnSerSerSerLeu 798 	9 PheLysSerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAla 778 	9 TyrCysValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAla 758 	9 ThrileProGlnAspArgLeuThrGluVallleAlaSerIleIleLysProGlnAsnThr 738 	9 AlaGInAspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAsp 718 	/2-2 (1-1132) x BM453198 (1-925)	Cores: 2.2e-87 Length: 925 1406.00 Matches: 274 11arity: 98.92% Conservative: 0 Similarity: 98.92% Mismatches: 1 23.59% Indels: 2 4 Gaps: 0

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU702370
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU702370 851 bp mRNA UI-M-FIO-byx-f-12-0-UI.rl NIH_BMAP_FIO Mus IMAGE:6400523 5', mRNA sequence.
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                                                       AlaPheLysSerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVal 777
                                                                                                                                              ThrTyrCysValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLys
                                                                                                                    ACGTACTGTATCCGCCAGTATGCAGTGGTCCGGAGAGATAGCCAAGGCCAAGTCCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="DH108 (TI phage resistant)"
/clone lib="NIH BMAP FIO"
/c
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/strain="C57BL/6"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                 1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mus musculus (house mouse)
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Rodentia;
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Sciurognathi; Muridae;
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    jies, Inc.
Consortium
                                                                                                                                         Collection (MGC)
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IMAGE:4949887 5',
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Clone distribution: MGC clone distribution information can
IleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSer 1055
                                                                                                                                                                                  TCGGTCT
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                                                           ThrValCysThrAsnIleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCys
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                                                                                      ValLeuGlnLeuProPheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgVal
                                                                                                                        /clone lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female, virgin"
/tissue_type="infiltrating
/dev_stage="5 months"
/lab_host="DH10B"
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'strain="FVB/N"
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BM824748
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 99 row: B column: 07
High quality sequence stop: 492.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (20)
Contact: Kim YS
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21C Frontier Korean EST Project 2001
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Kim, N.S., Hahn, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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             /note=Torgan: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean pattents by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                   clone_lib="S22SNU16n1"
                                                                                                                                                                                                                                                            cell_type="Lymphoblast-like"
cell_line="SNU-16"
                                                                                                                                                                                                                                                                                                                                                clone="S22SNU16n1-99-E07"
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                         tissue_type="Ascites"
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Percent Similarity: Best Local Similarity:

5.07e-44 776.00 100.00% 100.00% 13.02%

Length:
Matches:
Conservative:
Mismatches:
Indels:

492 148 0 0

Score:

Alignment Scores: Pred. No.:

Query Match:

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NISC kp11g04.q3 Baker mouse embryo IMAGE:5409222, mRNA sequence.
BQ258274
BQ258274.1 GI:20459030
                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
cDNA Library Preparation: J. Baker (Stanford University)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 664)
                                                                                                                                                                                                                 Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                         info@image.llnl.gov
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                                                                                                                                                                                    Cione distribution: NCI-CGAP clone distribution ound through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                         primer: Sp6 primer
                                                                                                                                                                                                                                                                                                                                   Gene Index
                                              /organism="Mus musculus"
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                                                                                                           Location/Qualifiers
                                                                                              .664
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Query Match:
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Tetraodon nigroviridis
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                                                                 CAGAAGAACAGGCTCTTCTTACCGTAAGAGTGTGTGGGAGCAAGCTG
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/lab_host="%I1-Blue"
/clone lib="Baker mouse embryo e7.5"
/clone lib="Baker mouse embryo e7.5"
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made by oligo-dT priming. Directionally cInned into
Sal1/Not1 sites using the following 5' adaptor:
5-TCGACCACGCGTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."
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771.50
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64.83%
12.94%
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full-length
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Conservative:
Mismatches:
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CR688161.1
HTC; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/tetraodon.
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Tetradontoidea; Tetraodontidae.
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                                                                                                                                                                                                             HisAlaLysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValVal
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                           AATCTCGACATCTATAAAGACTATTCTAGCTATGCAAACCTGTCCTTGCGCTACAGCCTT
                                                                                                                                                      AsnLeuArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAla
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ThrPheAsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGjyValLeu 978
                                            ThrLeuGluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu
                                                                               PheValGlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArg
                                                                                                                                      AATCCTCAGAAGATTGTGGTCAATTTTGAGGATTCTGAGAGCACAAACTCTTGTCCTGGC
                                                                                                                                                                                                                                                                   ArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Tetraodon"
/mol_type="mRNA"
/db_xref="taxon:47144"
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full-length; Tetraodon nigroviridis.
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682.00
58.36%
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Mammalia; Eutheria;
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CF531069.1 GI:34583033
                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                                                                                                                                  primer: pYX-5
                                                                                                                                    ocation/Qualifiers
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Email: cogapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF531069 649 bp mRNA linear EST 12-SEP UI-M-FY0-cgp-c-19-0-UI.rl NIH_BMAP_FY0 Mus musculus cDNA clone IMAGE:30355746 5', mRNA sequence.
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National Institutes of Health, Mammalian
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/moltype="mRNA"
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/db_xref="c57BL/10090"
/clone="IMAGE:30355746"
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="OH10B_(T1_phage_resistant)"
/clone_lib="NIH_BMAP_FY0"
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Rodentia;
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FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 11 CF531121 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 36 Db 62	σω	Qy 32	Qy 30 Db 55	Qy 28 Db 55	Ωy . 26		Оу 24	Db 54
Seq primer: pxx-5. 1688 /organism="Mus musculus" /mol_type="mgNA" /strain="C57BL/6" /db_xref="taxon:10090" /dt xref="taxon:10090" /clone="IMAGE:30355988" /tissue_type="whole brain" /dev stage="embryo 13.5,14.5,16.5,17.5dpc" /lab_host="DH10B (T1 phage resistant)" /clone_lib="NIH_BMAP_FYO" /note="Organ: Brain; Vector: pxx- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT	utheria; Rodentia; Sciurognathi; Muridae; Murinae to 688 p://mgc.nci.nih.gov/. ps://mgc.nci.nih.gov/. nstitutes of Health, Mammalian Gene Collection (MG 1 (1999) bert Strausberg, Ph.D. bbs-remail.nih.gov urement: Dr. Jim Lin, University of Iowa ury preparation: Dr. M. Bento Soares, University of iry preparation: Dr. M. Bento Soares, University of iry preparation: Dr. M. Bento Soares, University of Iowa ncing by: Dr. M. Bento Soares, University of Iowa ncing by: Dr. M. Bento Soares, University of Iowa mc.ulowa.edu/distribution/mousefl.html swas contributed by the Brain Molecular Anatomy F	688 bp mRNA linear EST 12-SEP-2 -UI.rl NIH_BMAP_FYO Mus musculus cDNA clone mRNA sequence. 33085 s mouse)	1 ValGluThrIlePheLeuGly 367 27 GTGGAGATCATCTTCTGGGC 647	1 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 36	1 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluG o	11 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320 	31 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300	57 557	6	11 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaH1sProGly 260	45 545

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Best Local Similarity: Query Match: DB: US-10-044-692-2 (1-1132) x CF531121 (1-688) Percent Similarity: Alignment Scores: No.: 559 379 319 583 241 221 201 181 161 499 141 439 121 101 259 199 139 81 61 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 21 79 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180 |||||| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu GTGGCCAGGGTTGTGCAGAGACTCTGCGAGCGCAACGAGAGAAACGTGCTGGCTTTTGGC ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrp-AlaHisProGl ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu GGCTCACAGCCTGCCGACCTTTCCTTCCACCAGGTGTCATCCCTGAAAGAGCTG GTGTGGCCGCTGGCAACCTTTGTGCGGCGCCTGGGGCCCGAGGGCAGGCGGCTTGTGCAA AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg CTGGTGCCCCCCAGCTGTGCCTAC-----AGCTACTTGCCCAACACTGTTATTGAGACCCTGCGTGTCAGTGGTGCATGGATGCTACTG PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator." 3.45e-36 666.50 46.34% 41.73% 11.18% Indels: Gaps: Length: Matches: Conservative: Mismatches: CAGGGGAGATGGCCAN----688 154 17 32 36 166 220 160 598 240 200 498 140 438 120 198 40 582 582 582 558 378 318 80 258 60 138 20 REFERENCE AUTHORS AA281296 LOCUS 밁 5 밁 Ś 밁 δ 멍 Ş 밁 S 밁 S ORIGIN FEATURES COMMENT SOURCE RESULT 12 VERSION ACCESSION DEFINITION KEYWORDS JOURNAL TITLE ORGANISM source 664 360 604 340 599 320 598 300 280 260 yArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGl Thuor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 385. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens mRNA sequence zt08g02.r1 AA281296.1 GI:1924194 AA281296 Homo sapiens (human) GGTGGAGATCATCTTTCTGGGCTCA uValGluThrIlePheLeuGlySer 368 TCTAAACCCCTCATTCCTACTCAGCANCCTCCAGCCTAACTTGACTGGGGGCCAGGAGACT nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe uGluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGl оСувРroProValTyrAlaGluThrLyвНівРheLeuTyrSerSerGlyAврLyвGluGl yArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPr (bases 1 to 389) Location/Qualifiers /tissue_type="germinal center B /lab_host="DH10B" /clone="IMAGE:712562" mol_type="mxwa"

'db_xref="taxon:9606" organism="Homo sapiens" /mol_type="mRNA" 389 bp mRNA linear EST 14-AUG-1997 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', 688 ce11"

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                                                                                                                                                                                                        Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sanao, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB618671 S99 bp mRNA linear BB618671 RIKEN full-length enriched, 8 days embryo cDNA clone 5730412M20 5', mRNA sequence.
                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of Capt-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB618671.1 GI:16458173
                                                                                                       Fax: 81-45-503-9216
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1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu

Gaps:

21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln

40 174 20

60 234

ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp

AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80

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Percent Similarity:
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KONDO, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Konno, H., Fukunishi, Y. Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Sugahara, Y. and Hayashizaki, Y.

Sugahara, Y. and Hayashizaki, Y.

Genome Res. 11 (2) 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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/lab_host="DH10B"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,
Lebkowski,J and Stanton,L.W.
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409 bp mRNA linear EST 16
17000531326763 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 409 Std Error:
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230 Constitution Drive, Menlo Park,
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/note="oligo dT primed, full-length enriched cDNA library
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hBS cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMB748 row: h column: 07
High quality sequence stop: 639.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE371943 866 bp mRNA linear EST 21-JUL-2000 BE371943 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheAlaLeuLeuAspGlyAlaArgGly 109
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                                                                                                                                       /clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                               /clone="IMAGE:3586614"
/tissue_type="spontaneous tumor,
Stem cell_origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                              1. .866
                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
4.72e-29
566.00
82.31%
73.47%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 bp mRNA
BB651920 RIKEN full-length enriched, ES
clone C330020G14 5', mRNA sequence.
BB651920
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                   Fax: 81-45-503-9216
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Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashiazki, Y. and Hayashiazki, Y. and Hayashiazki, Y. (2000) [1], 1757-1771 (2000) [2], Nonno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (2001) [2], 281-289 (20
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355 GTGGCCAGGGTTGTGCAGAGACTCTGCGAGCGCAACGAGAGAAACGTGCTGTTTTGGC 414	81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100	295 GGCTCACAGCCTCCACCTGCCGACCTTTCCTTCCACCAGGTGTCATCCCTGAAAGAGCTG 354	61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80	235 CCCGGGGACCCGAAGATCTACCGCACTTTGGTTTGCCCAATGCCTAGTGTGCATGCA	41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60	175 GTGTGGCCGCTGGCAACCTTTGTGCGGCCCTGGGGCCCGAGGGCAGGCGGCTTGTGCAA 234	21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40	115 ArGACCCGCGCTCCTTGCCCCGCGGTGCGCTCTCTGCTGCGCAGCCGATACCGGGAG 174	1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20	US-10-044-692-2 (1-1132) x BB651920 (1-614)

1.91e-28 554.00 82.67% 75.33% 9.29%

Length:
Matches:
Conservative:
Mismatches:

614 113 11 25 0

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FORWARD: 5 CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' |
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3'
Insert Length: 1 Std Error: 0.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oldspouncleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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Genome Res. 13 (6A), 1056-1066 (2003)
22683279
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New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
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Branchiostoma floridae
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Contact: Panopoulou G
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The library was characterised by oligonucleotide fingerprinting
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/tissue_type="whole embryo"
/dev_stage="26 hrs (neurula stage)"
/dev_stage="2.6hrs (neurula stage)"
/lab_host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
/state="taxon:100531)"
/state="taxon:100531)"
/state="taxon:100531"
/state="taxon:100531"
/note="Vector: pSport1 (Gibco BRL); Site_1: Sall, KpnI,
EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT
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primed and directionally cloned in pSport1 vector using a NotI.(5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC (T)15-3' and a Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."

lignment Sco	res:
Score: Score: Sercent Simil Best Local Si Query Match: DB:	1.01e-25 Length: 75 517.00 Matches: 110 517.00 Matches: 100 Similarity: 42.80% Mismatches: 104 Similarity: 42.80% Indels: 6 Gaps: 2
JS-10-044-6	92-2 (1-1132) x BI388013 (1-775)
¥ ¥	16 HisalaValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySer 835
λy 83	36 IleLeuSerThrLeuLeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAla 855
¥	81 TGCCTGTCCACCCTGCTCTGTAGCTTCTTCTACGCTAACATGGAGAGAGA
<i>y</i>	56 GlyIleArgArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrPro 875
ъ 1	41 GGCATGGACATGGATGGGTTGCTGCTGCTGCTGGTGATGACTTTCTGCTGGTGACCCCA 200
אל	76 HisleuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValProGluTyrGly 895
)b 2	01
8	96 CysValValAsnLeuArgLysThrValValAsnPheProValGluAspGluAlaLeuGly 915
ъ ъ	61
γ 9	16 GlyThrAlaPheValGlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeu 935
)b 3	12 AATGCTGTGGTGACATGTCAGCCAGCAGTCGGCTGGTTCCCGTGGTGCGGCATGCTGTTC 371
9	36 AspThrArgThrLeuGluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArg 955
ъ 3	72 CACACTCTCCTGCTAGGGGTCATGAGAGAGTACACAAAATATGCCCAACCTGAGTATCAGG 431
γ γ	56 AlaSerLeuThrPheAsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPhe 975
ъ ф	32 TACACTTTGACCTTTGACCTCCATCAGACTCCCGGTCAGGCCATGAAACAGAAGCTGATG 491
y y	76 GlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGln 995
)b 4	92 AACACTGTCAAGGCCAAGTGTCATGCCTTCTTCCTGGAGCCCCAAGGTGAATTCAGCAGCT 551
) 9	96 ThrValCysThrAsnIleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCys 1015
5	52 GTGATTCAACAGACTCTCTACAAGGCATTCCTGTTCACAGCCCCACCAGCTTCCACAGCTAC 611
)Y 101	16 ValLeuGlnLeuProPheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgVal 1035
6 طر	12
λγ 10	36 IleSerAspThrAlaSerLeuCysTyrSer
ъ ъ	TCATGGACATCTGCCATTACCCCCTTCTACTGGTTGATGCAATGGTGGC
λλ 10	56 LeuGlyAlaLysGlyAlaAlaGlyProLeuProSerGluAlaValGlnTrp 1072 -:-
)b 7	23 AAGAAAGTGATGTCAGGGCAGCTTCCTGTATCCCAAGATGCANTANAATGG 773
RESULT 18 3U452535 LOCUS	BU452535 753 bp mRNA linear EST 29-NOV-2002 603767927F1 CSEQRBN14 Gallus gallus cDNA clone ChEST696f7 5', mRNA
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1 (bases 1 to 753)

1 (bases 1 to 753)

1 (Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs (curr. Biol. 12 (22), 1965-1969 (2002)
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Department of Biomolecular Sciences
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AsnProThrPhePheLeuArgVallleSerAspThrAlaSerLeuCysTyrSerIleLeu
                                                                                                                                                                                     GACTTAAAGATCAACAGCCTTCAGACAGTTCTAATTAACATCTACAAGATATTTTTACTT
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/clome_lib="CSEQRBN14"
/clome_lib="CSEQRBN14"
/note="Togan: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Togan: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Togan: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Togan: ovary; Vector: pBluescript was
constructed from | million independent clones.cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
/note for first strand synthesis reaction.
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/lab_host="DH10B"
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/sex="Female"
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1 (bases 1 to 846)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Len Zon, Harvard
Tissue Procurement: Len Zon, House Consortium (LINL)
CDNA Library Preparation: Offer I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can if found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
http://image.llnl.gov
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National Cancer Institute / NIH.
Bldg. 31 Rm10A07 Bethesda, MD 20892
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/clone libe"NIH ZGC 7"
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
/note="Vector: pExpress1; Site_1: NotI = ndividual
from the Tuebingen strain. 1st strand cDNA was primed wi
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH_ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
                                                                                                                                                                                                                                                                                                                    /db xref="taxon:7955"
/clone="IMAGE:7267941"
/tissue_type="whole body"
/lab_host="DH10B"
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GluVal-GlnSerAspTyrSer------SerTyrAlaArgThrSerIleArgAlaSe
                                     AACAGCCCCACG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
/mol_type="mRNA"
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db_xref="taxon:9031"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 880)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                   GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu
                                                                                                                                                                                      AGCTTAÁCÁGAAAATÁÁCTTCAAACTGGÁGGÁTAATATNGTA-----GTTTTGTCTATA
                                                                                                                                                                                                                                                                                                                   AAAAACTTTATAGGCACTTTG---AAAGGACCCCTAGAGATGGCATTAGACATTTCTCAA 152
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KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1966): 791, except that a significantly longer reannealing hybridization was used."
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659344 NCCCWA 1RT
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Rexroad,C.E. 3rd, Lee,Y., Keele,J.W., Karamycheva,S., Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
Sequence analysis of a rainbow trout cDNA library and
                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
                                                                                                                                                                    USDA, ARS, National Center for Cool and Cold Water 11876 Leetown Road, Kearneysville, WV 25430, USA Tel: 304 724 8340 x2129 Fax: 304 725 0351
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                           Seq
                                                                                                                         Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
                                                                                                                                                                                                                                                    Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
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                                                                                           ss match v0.990329.
primer: AGCGGATAACAATTTCACACAGGA
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organism="Oncorhynchus
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT49P11_B_H06"
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/lab_host="DH10B"
/clone lib="NCCCWA 1RT"
/clone lib="NCCCWA 1RT"
/note="Vector: pcMV SPORT6; Site 1: NotI; Site 2: SalI;
/ibrary made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."
              'n
                                                          tcbk Oncorhynchus
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Campus de beaulieu, l
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Plate: 00
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
On Dec 18, 2003 this sequence version replaced gi:40140362
Contact: Guiguen Y
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 724)
Govoroun, M., Guiguen, Y. and Le Gac, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
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 SerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGlu
                                                           ThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGln
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                                                                                                                                                                                                                  GCTGAGCTGATGTGGAAGATGAAGGTGAATGACTGTGATTGGCTGAAGATCAGCAAG---
                               AGCATGGGACAGAAGAACGCACTGCGCTTCTACAGATACCAGGTCTGGGCCCAAGCTGCAG
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/tissue_type="multi-tissues"
/tissue_type="from_embryos to
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                                                                         /mol_type="mRNA"
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/clone="1RT74012_C_H06"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                     organism="Oncorhynchus
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 632)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G., Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J. Sequence analysis of a rainbow trout cDNA library and creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
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/note="Vector: pCMV SPORTG; Site_1: NotI; Site_
Library made from pooled tissue from brain, gil
spleen, muscle, and kidney."
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                                                                  BE396925
601290610F1 NIH_MGC_8 Homo sapiens
            Homo
                      EST
                                   BE396925
BE396925.1 GI:9342290
  Homo
                                                           mRNA sequence.
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AGGAAGCTCATGTCCATTCTTAGATTCAAGTGCCACGCCCTCTTCCTGGACCTCAGAACC 561
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7.54%
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REFERENCE
AUTHORS
TITLE
JOURNAL
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM294 row: c column: 03
High quality sequence stop: 634.
Location/Qualifiers
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1 (bases 1 to 715)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
       BX886589
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/clone="IMAGE:3621050"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="Burkitt lymphoma"
/lab host="Burkitt lymphoma"
/clone lib="NIH MGC 8"
/clone lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
703 bp mRNA linear EST 27-JUL-2004 tcbk Oncorhynchus mykiss cDNA clone tcbk0036c.p.02 5prim,
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TITLE
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INRA - SCRIBE
Campus de beaulieu, J
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
On Dec 18, 2003 this sequence version replaced gi:40135983
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Construction and primary characterization of normalized cDNA
Libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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EST.
CysValLeuGlnLeuProPheHisGlnGlnValTrpLysAsnProThrPhePheLeuArg
                                                                GAGGCTGTCTATAGCAACGTCTATAAGTTAGTGTTGCTGCAGGCGTTCAGGTTCCATGCC
                                                                                     GlnThrValCysThrAsnIleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAla
                                                                                                                                                                                                                                                                                                            CTGAATACACACCCTGGACGTCTA-CACAACTACGCCAGCTACGCTGGCCTATCCCTG
                                                                                                                                               ATGTCCATCCTTAGATTCAAGTGCCACGCCCTCTTCCTGGACCTCAAAACCAACTCCCTG
                                                                                                                                                                                      PheGlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeu
                                                                                                                                                                                                                               CGCTACAGCCTGACGCTAGGCTCCGCCCCACTGCGCGGGCAGCAAATGAAGAGGAAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=TVector: pT7T3D-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.28.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="tcbk0036c.p.02"
/tissue_type="multi-tissues"
/dev_stage="from_embryos to adults"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Oncorhynchus mykiss"
|mol_type="mRNA"
|db_xref="taxon:8022"
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437.00
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48.47%
7.33%
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Conservative:
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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 344)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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EST.
Mus musculus (house mouse)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAGACAGGCTGCCACACCCCAAAATGCCTGAAGACTTCAAGGCCATC
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/dev stage="mobity" 13.5,14.5,16.5,17.5dpc"
//lab_host="DH10B (T1 phage resistant)"
//clone lib="NIH BMAP FY0"
//clone lib="NIH B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="whole brain"
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REFERENCE
AUTHORS
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Best Local Similarity:
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JOURNAL
MEDLINE
PUBMED
                                                                                      TITLE
                                                                                                   RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Khite, O., Cline, T.R., Cotton, M.D., Earle-Hughes, J. Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fricchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
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                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 409)
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EST182469 Jurkat T-cells
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Seq primer: M13 Ryerse.
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                                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
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9712 Medical Center Drive, Rockville, MD 20850 USA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
cDNA Library Preparation: Ling Hong/Rubin
                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                          BE396606 67
601289077F1 NIH_MGC_8 Homo
                                                                                                                                                                                                              BE39660
                                                                                                                                                                                                BE396606.1 GI:9341882
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/mol_type="mRNA"
/db_xref="ATCC (inhost):158964"
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/clone_lib="Jurkat T-cells VI"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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/cell_type="T-lymphoc
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                                                                                    BUIl1946.1 GI:25315846
EST.
Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasiphasianinae; Gallus.

1 (bases 1 to 835)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM290 row: i column: 19
High quality sequence start: 2
High quality sequence stop: 656.
Location/Qualifiers
                                                                                                                                                                                                                            BU111946
                                                                                                                                                                                                                                               sequence.
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/lab_host="DH10B (phage-resistant)"
/clone_libe="NIH_MGC_8"
/clone_libe="NIH_MGC_8"
/clone_libe="NIH_MGC_8"
/clone_libe="NIH_MGC_8"
/cloned_into_BcoRI/Xhol sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Simon.Hubbard@umist.ac.uk
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 rIleIleLysPro----:
                                                                              lAspValThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluValIleAlaSe
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                                                      TGATGTATCCAGAGCTTTTGATACCATTCCTCACAAGAAACTTGTGGAAGTGATATCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: limbs; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaaag] [5'aattcttttttcggatccgggctgcacgc]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="ChEST98p18"
/dev_stage="22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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-GlnAsnThrTyrCysValArgArgTyrAlaValValGlnLy
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Matches: Conservative:

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Gaps: Indels: Mismatches:

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM330 row: f column: 19
High quality sequence stop: 628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 649)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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601316575F1 NIH_MGC_8 Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 649)
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                                                                                                    /tissue_type="Burkitt lymphoma"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone lib="WIH MGC B"
/clone lib="WIH MGC B"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
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/cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
California, Berkeley) using ZAP-CDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                     (Stratagene) and Superscript
                                                                                                                                                                                                                                                                                                                 clone="IMAGE:3634962"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Clone distribution: MGC clone distribution, at: image.llnl.
                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM330 row: g column: 20 High quality sequence stop: 610. Location/Qualifiers
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1 (bases 1 to 610)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="Burkitt lymphoma"
/lab host="BH10B (phage-resistant)"
/clone_lib="NIH_MGC ##
/clone_lib="NIH_MGC ##
/clone_lib="NIH_MGC ##
/cloned into made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                   /clone="IMAGE:3634987"
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cDNA clone IMAGE:3634987

linear

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Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Galliformes; Phasianidae;
Eukaryota; Mecazoa; Chordatae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae; Galliformes; Phas
phasianinae; Gallus.
1 (bases 1 to 696)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Carr. Biol. 12 (22), 1965-1969 (2002)
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603134527F1 CSEQCHL24 Gallus
                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 Tel: 01612008930
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                                                                                                                                                                                                                                                                                                                              Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
                 /clone lib="CSEQCHL24"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and
                                                                                                                                                                                                                                     /organism="Gallus gallus"
/mol type="mRNA"
/strain="Whitte Lephorn, Hisex"
/db_xref="taxon:9031"
                                                                                                                                                                                 /dev_stage="16 day embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                     clone="ChEST116f8"
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Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Alzawa, K., Arakawa, T., Ishil, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuhhi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Muramatau, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Muramatau, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
                                                                                                                                                                                                                                                                                                                                                BY783093 343 bp mRNA linear EST 23-MAR-20
BY783093 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930172A03 5', mRNA sequence.
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1 (bases 1 to 343)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mus musculus (house n
Mus musculus
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Please visit our web
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Fax: 81-45-503-9216
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Mus musculus cDNA clone L930188J05 5',
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Ri Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed
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/mol_type="mRNA"
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Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Rikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Pavan, W., Shinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatesu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY775178 RIKEN full-length enriched,
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Mammalia; Eutheria; Rodentia;
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'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="L930091N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="mRNA"
                                                                                                                                                                                                                                             9.38e-17
380.00
85.00%
77.00%
6.37%
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Sciurognathi;
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AW244516/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGln 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 GlyProProGluAlaPheThrThrSerValArgSerTyrLeuProAsnThrValThrAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequencing by: University Core DNA Services, University of calgary. Submitted sequence has been trimmed at both ends to remove the adaptor oligos containing the EcoRI sites; i.e. GAATTCGGACTA (beginning) and TAGTCCGAATTC (end) removed. Therefore, reported insert length is longer than actual EST sequence length. Insert Length: 359 Std Error: 10.00 Seq primer: T3.0r.T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biochemistry and Molecular Biology University of Calgary 3330 Hospital Drive N.W., Calgary, Alberta, T2N Tel: 403 220 2888 Fax: 403 283 8727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BR_END06B09 Bain Rancourt retinoic acid induced ES cell neural differentiation subtraction library Mus musculus cDNA clone 06B09 similar to gb|Ap0703311|Ap0703311 Mus musculus telomerase catalytic subunit mRNA, complete cds, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bain, G., Mansergh, F.C., Wride, M.A., Hai
Rancourt, S.L., Ray, W.J., Yoshimura, Y.,
and Rancourt, D.E.
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Mammalia; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rancourt@ucalgary.ca; URL:http://www.acs.ucalgary.ca/
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        /clone lib="Bain Rancourt retinoic acid induced ES cell neural differentiation subtraction library"
/note="vector: pBluescript II SK+ (Stratagene); Site_1: EcoR1; Site_2: EcoR1; Library constructed by Dr. Gerard Bain (present address: Hoechst-ARIAD Genomic Center, ARIAD Pharmaceuticals Inc., 26 Landsdowne Street, Cambridge, Massachusetts, 02139-4234, U.S.A.). To isolate cDNAs corresponding to mRNAs which are upregulated during the neural differentiation of ES cells in vitro, the subtractive hybridization technique of Wang and Brown [1] was employed. Poly(A)+ RNA was prepared from both undifferentiated ES cells and from embryoid bodies which had head neural track for Asam in the absorbed for follows.
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                                                                                                                                                                                                                                                                                                                                                                 /cell_type="embryonic stem
/cell_line="D3"
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had been cultured for 4 days in the absence of RA followed
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Rodentia;
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Y., Tsuzuki, T., Gottlie
                                                                                                                                                                                                                                                                                                                                                                                                (ES) cell"
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US-10-044-692-2 (1-1132) x AW244516 (1-347)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                  LeuAsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAla 817
                                                                                                                                                                                                                                                                                                                                                                             LeuGlnGluThr-----SerProLeuArgAspAlaValValIleGluGlnSerSerSer 797
                                                                                                                                                                                                                                                                                                                                                                                                                                    LysSerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHis 779
                       ĠŢŖŖŖĠŢŢĠĠŢĠŖĊŖĠĠŢĠĊŢŖŢŖĊĠĊŖĠĠĠĊŖŢĊĊĊĊŔĠĠĠĊŢĊĊŖĠĊĊŢŖ
                                                                                                                                            ValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeu 837
                                                                                                                                                                                                                  ATGAATGAGAGCAGCAGCCTGTTTGACTTCCTTCCTGCACTTCCTGCGTCACAGTGTC 106
                                                                                                                                                                                                                                                                                                                         TCCACCCTGCTGCAGTCTGTGTTTCGGAGACATGGAGAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Gibco). Aliquots of Doth CUNMAS were clysted with the restriction enzymes AluI and AluI plus Real. An adaptor oligo [1] containing an EcoRI site was ligated to the ends of the restricted CDNAs to provide primer binding sites and large amounts of each cDNA population were then produced by the polymerase chain reaction (PCR) as described [1]. Amplified cDNA from undifferentiated ES cells was biotinylated using Photoprobe biotin (Vector Laboratories) according to the manufacturer's protocol.

2.5 ug of amplified cDNA from 4-/3+ cells was mixed with 50 ug of biotinylated ES cell cDNA, denatured by boiling, and hybridized for 20 h. Double stranded cDNAs containing biotin were removed by streptavidin/phenol treatment as described [1]. The remaining subtracted cDNA was mixed with an additional 25 mg of biotinylated ES cell cDNA, denatured by boiling, and hybridized for 2 h. The streptavidin/phenol treatment was repeated and the remaining cDNA was amplified by PCR [Wang and Brown, 1991]. Two additional rounds of subtraction were repeated to pBS II SK+ (Stratagene) followed by transformation into E. coli DH5 cells. Individual colonies were picked and the corresponding plasmids were isolated either by an alkaline lysis miniprep procedure [2], or using the gardencer (University Core DNA Services, University of Calgary). 1. Wang, 2. Brown, DD (1991) A gene expression screen. Proc. Natl. Acad. Sci. USA 88, 11505-11509. 2. Sambrook, J; Fritsch, EF; Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York."
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RS Okazaki, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Rikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegdawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegdawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegdawa, Y., Nogami, A., Matsuda, H., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. M., Blake, J. A., Bradt, D., Brusic, V., Bratio, C., Godosti, J., Schriml, I. M., Kanapin, A., Matsuda, H., Bratic, V., Bratic, C., Godostik, A., Gough, J., Grimmond, S., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T. A., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kunghi, H., Kawasawa, Y., Kedziarski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D.R., Kawaiji, H., Karasawa, Y., Kedziarski, R.M., King, B.L., Konagaya, A., Namata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Peta, M., Maltais, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdate, R.D., Tomita, M., Varardo, R., Wang, I., Wallestedt, C., Wang, Y., Watanabe, Y., Yang, I., Wallestedt, C., Wang, Y., Watanabe, Y., Yang, I., Wallestedt, C., Wang, Y., Watanabe, Y., Yang, I., Makawa, T., Fukuda, S., Hara, A., Hashizume, W., Ishihi, Y., Ithoh, M., Kangawa, I., Miyazaki, A., Sakai, K., Kawai, K., Ishihi, Y., Anakawa, T., Fukuda, S., Hara, A., Hashizume, W., Ishihi, Y., Anakawa, T., Konno, H., Nakamura, M., Shihata, K., Sakai, K., Sasaki, D., Shibata, K., Shihaki, Y., Sakai, Y., Sasaki, D., Shibata, K., Shihaki, Y., Sakai, Y., Sa
                                                                                                                                                                                                                                                                                                                Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akmura,T., Arakawa,T., Carninci,P., Pukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

**RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-922
Fax: 81-45-503-921
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Please
further
Contact: Robert B. University of Utah University of Utah
                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 641)
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641 bp DNA linear GSS 2: 2M0246F07F Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0246F07 F, genomic survey sequence.
                                        plasmid inserts
Unpublished (2000)
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GSS.
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                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse tissues.
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/dev stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
whole body"
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|strain="C57BL/6J"
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374.00
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High quality sequence stop: 641.
Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0246 row: F column: 07
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Cold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. coli strain XL10-Gold, T1-resistant, /clone lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: PWD42nv; Purified genomic DNA from Nusculus C57BL/6J (female) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/).
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strain="C57BL/6J"
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CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAsp---LysGlu
                                              ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro
                                                                                                         AAAGATTTGTCTTCTAAAGGAAAGGTGTCTGACCTGAGTCTCTCT----GGGTCGGTGTGC
                                                                                                                                    GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly
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619 bp mRNA linear EST 29-DEC-2003 K0850A03-5 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence. CK392784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                        Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnælgsun.grc.nia.nih.gov
Plate: K0850 row: A column: 03
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High quality sequence st
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                                                                                                                                                                                                                                                                          quality sequence stop: 619
                                                                db xref="taxon:10090"
/clone="NIA:K0850A03 IMAGE:30083138"
/tissue_type="whole embryo including
tissues at 8.5-days postcoitum"
                                                                                                                                                                                                                                    Location/Qualifiers
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/strain="C57BL/6J"
/clone lib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) "
                                  /dev_stage="8.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                            db_xref="niaEST:K0850A03-5"
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by Yulan Piao (NIA)."

	Qy 343 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 362 ::: ::: :::	Qy 324 ValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 342 :::	Qy 304 HisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysProPro 323	QY 284 SerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGlnHis 303	QY 269 GlyPheCysValValSerProAlaArgProAlaGluGluAlaThr 283 :::	Qy 249 ThrProValGlyGlnGlySerTrpAlaHisProGlyArgThrArgGlyProSerAspArg 268	Qy 229 SerArgSerLeuDroLeuDroLysArgDroArgArgGlyAlaAlaProGluProGluArg 248	Qy 209 GluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArgArgArgGlyGlySerAla 228	US-10-044-692-2 (1-1132) x CK392784 (1-619)	Alignment Scores: 2.24e-15 Length: 619 Pred. No.: 366.00 Matches: 97 Score: 55.61% Conservative: 22 Percent Similarity: 45.33% Mismatches: 79 Best Local Similarity: 45.33% Indels: 16 Query Match: 7 Gaps: 6
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US-10-044-692-2 (1-1132) x BE268183 (1-779) Qy	ORIGIN California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." Alignment Scores: Pred. No.: 1.24e-14 Length: Scores: 957.50 Matches: 16 Best Local Similarity: 44.44* Mismatches: 50 Query Match: 50.57* Conservative: 16 Ouery Match: 50.59* Conservative: 16 Gaps: 9 Gaps: 9	/organism="Homo sapiens" /mol type="mRNA" /db xref="taxon:9606" /clone="tyAGE:3345111" /tissue_type="Burkitt lymph/ tissue_type="Burkitt lymph/ /lab host="DH108 (phage-res /clone_lib="NHH MGC 8" /note="Organ: lymph; Vector EcoRI; cDNA made by oligo-de cloned into EcoRI/XhoI site adaptor: GGCACGAG(G). Size insert size 1.8kb. Library	Email: Cgapbs-remail.nin.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Flatte: LLCM132 row: i column: 16 Plate: LLCM132 row: i column: 16 Plate: LLCM132 row: i column: 16 FEATURES FOURCE 1779	Eukaryo Mammali 1 (bas NIH-MGC Nationa Unpubli Contact	RESULT 40 BE268183 BE268183 BE268183 TOCUS BE268183 BE268183 BE268183 BE268183 VERSION BE268183.1 GI:9141784 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human)	Db 513 TCGCGTCGATACTGGCAGATGCGGCCCCTGTTCCAACAGCTGCTGGTGAACCATGCAGAG 572 Qy 403 CysProTyrGlyValLeuLeuLysThrHisCysProLeuArg 416
Ω e	VERSION VERSION HOLZZ97/.1 G1:2332991 KEYMORDS GST. SOURCE Gallus gallus (chicken) ORGANISM Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus REFERENCE Phasianinae; Gallus REFERENCE AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. TITLE A Comprehensive Collection of Chicken cDNAs JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)	710CCTAGTCGTCGGGCCAAAAGGTC 662 eSerValLeuAsnTyrGluArgAlaAr 737GAAAGGGCGGG 7 BU122597 10N 603148441F1 CSEQCHL18 Gallus sequence ON BU122597 ON BU122597	Oy 603 luAlaGluValArg-GlnHisArgGluAlaArgProAlaLeuLeuThr-SerArgLeuAr 804	Oy 566 ThrThrPheGlnLysAspArgLeuPhePheTyrArgLysSerValTrp-SerLysLeuGl 585	Db 309 CGGGGTGACGTCACCAGGCCCTCGGTGATGTGGCATGTCCTTCTCTTTAAGGG 368 Oy 526 ValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeu 545	500 HisalaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArg

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US-10-044-692-2 (1-1132)
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                                                                                                    oLeuTyrGlnLeuGlyAlaAlaThrGlnAlaArg-ProProProHisAlaSerGlyProA
                                                                                                                                                                            aArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGlnValCysGlyProPr
                                                                                                                                                                                                                                              GlyAlaTrpGlyLeuLeuArgArgValGlyAspAspValLeuValHisLeuLeu-Al
                                                                                                                                                                                                                                                                                      CCATCTTCGTGTATATACAGCTATCTGTCCAATACTGTAACAGAAACGATTCGGATCAGT
                                                                                                                                                                                                                                                                                                                   PheThrThrSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArgGlySer
                                                                                                                                            GGCCTCTGGGAGATACTGCTGAGTÄGGATAGGGGACGÄCGTGATGATGTACCTGCTGGAG
 GACGACGGTACTCA---
                                rgArgArgLeuGlyCysGluArgAlaTrpAsnHisSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=Torgan: small intestine; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: Not1; Modification of pBluescript II Ke(+); Step 1: EcoRI; Site 2: Not1; Modification of pBluescript II Ke(+) [Strategene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagcccggatccggaaaaaaag] [5'aattctttttttcggatccggatccggaacagc] "
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/clone="ChEST151a12"
/sex="Female"
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                                                                        --ATTTCGCGTAACCGTAGGGCCATCCCCA-----
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930 bp mRNA linear EST 09-JUN-2004
EST802411 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEC236 5' end, mRNA sequence.
CO014076
CO014076.1 GI:48520965
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
                                                                                                                                                                        4 GAAGTGAAGGAAGAAACGGCGGCCAGG-----ATCCTGTCGAGGAGGACCCTGGGCTAC
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Other_ESTs: EST802410
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Gardner, M.J. and Cole, G.T.
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ArgValLysAlaLeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeu
                                                                                                            GCACCCTTCGAATGCTCCCCAAGCGCACCGGAGCTCGTCCGATCGTTAACCTGAGAAAG
                                              CGCGCCATCGTCAAGTCCAGGTGGAATGGAAGGATAGAGCTGGGGCACAGTGCCAACACG
                                                                            AspTyrValValG1yAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSer
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2 Medical Center Drive, Rockville,
301 838 3519
301 838 0208
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/note="Vector: pExpress 1; Site 1: Not I; Site Coccidioides posadasii spherule CDNA library,
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/lab_host="E. coli DH10B,
/clone_lib="Coccidioides)
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strain="C735"
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AUTHORS
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Gardner,M.J. and Cole,G.T.
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides
spherules via expressed sequence tags
Unpublished (2003)
                                                                                                                                                                                                                                                    CO028055
983 bp mRNA linear EST 10-JUN-2004
EST806439 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone CIFAO39 3' end, mRNA sequence.
CO028055
CO028055.1 GI:48558725
                  9712
Tel:
                                                              Other_ESTs: EST806440
Contact: Gardner MJ
                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides
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                               The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850,
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   VallleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAla-----LysAsnAla 1052
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                                                 CGGCGGCAGCGGAACAGCCGAGAGGTGAGGAGGTCCTCGATGGACGACATGCTCACCCGC
                                                                                                             GTATATCACGCGTTCCTCGACTGTGCGATGAGGATGTATGCGTATCTGCGGTCGCTCTCG
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                                                                                                                                                                                                                                                                   AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu
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Location/Qualifiers
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/lab_host="E. coli DH10B, T1 phage resistant"
/clone l1b="Coccidioides posadasii spherule cDNA library,
0.5 to 5.3 kb"
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1023)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii spherules via expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO024489.1 GI:48551589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
Other_ESTs: EST802874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coccidioides posadasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Gardner MJ
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                                                                                                                 CACCTTGTGAAGATCGGGAAGAAGTATTTCGA-CAGAAGAACGGGATCCCGCAGGGCTCG
                                                                       IleLeuSerThrLeuLeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeu-----
                                                                                                                                  {\tt ThrProHisLeuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValProGlu}
                                        PheAlaGlyIleArgArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuLeuVal 873
                          TTCTTGGGCGGCGATGAAGAATCGCTCCTGCTGCGTCTGATCGACGACTACCTGCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute for Genomic Research
2 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 838 3519
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                            gardner@tigr.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            /note="Vector: pExpress 1; Site 1: Not I; Site Coccidioides posadasii spherule cDNA library, tb "
                                                                                                                                                                                                                                                                                                                          /Lab_nost="E. coli DH10B, Tl phage resistant"
/clone lib="Coccidioides posadasii spherule cDNA library,
).5 to 5.3 kb"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Coccidioides
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                   dev_stage="spherules"
lab_host="E. coli DH10B,
                                                                                                                                                                                                                                                                                                                                                                           clone="CIFA132"
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914 LeuGlyGlyThrAlaPheValGlnMet-----ProAlaHisGlyLeuPheProTrpCys 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 bp mRNA linear EST 22-1
AGENCOURT 15568263 NICHD XGC_Kid1 Xenopus laevis cDNA clone
IMAGE:7005014 5', mRNA sequence.
Bldg. 31 RM10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                             Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D
Office of Cancer Genomics
                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog)
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Strongylocentrotus purpuratus

Strongylocentrotus purpuratus

Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                       CD310596 687 bp mRNA linear EST 16-SEP-2003
StrPu691.003960 Sea urchin larva cDNA library MPMGp691
Strongylocentrotus purpuratus cDNA clone
MPMGp691N05127;MPI_SURUDI_127NS 5', mRNA sequence.
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Plate: LLAM14713 row: 1 column: 04
                                                                                                                                               CD310596
CD310596.1
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  Strongylocentrotidae; Strongylocentrotus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGTATGCATTCCAAGAGGAACAAAGCCGCTCCCGGTCCCCGGTCTCTTCAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerCysLeuLysGluLeuValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheThrThrSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArgGlySer 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGTTCTAGCTTTTGGTTATGGCTTAGTTGAT---GAAAAAAACTCACTGAATATTCGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus laevis"
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/db xref="taxon:835"
/clone="IMAGE:7009014"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC_Kid1"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.
Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.
Average insert size 2.2 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
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Oligo dT.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at http://www.molgen.mpg.de/ag_seaurchin/.cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
     736
                                               230
                                                                                                 720
                                                                                                                                                 173
                                                                                                                                                                                              700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP) 3'-seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Max-Planck-Institut fuer Molekulare Genetik
Ihnestr 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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laboraty 145, dept.Lehrach
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GlnAsnThrTyrCysValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisVal 755
                                                                                                                                                                             GlnAspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThr 719
;;;|||
                                                                                                                                                                                                                                                                                           LeuGlyLeuAspAspIle---HisArgAlaTrpArgThrPheValLeuArgValArgAla
                                                                                                                                                                                                                                                                                                                                        CTGTTTGATGTGTTGACATACCACAAAGTCAACCAGCCATCTGTGCTGGGCTCCTCCCTG
                                                  ATCAAGCATTCCAAGCTGCTACAGATTATCTCAATGCTTCTCCAAGGGCATGACAAGCCA
                                                                                                                                                 AAGGATACCAGACCG---CTGTACTTTGTGAAGATAGACATTGATAAGTGTTATGACTCC
                                                                                                                                                                                                                                              IleProGlnAspArgLeuThrGluValIleAlaSerIleIle--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: 5'-CCGGTCCGGAATTCCCCGGGT-3' pSport3/86
h quality sequence stop: 687.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MPMGp691N05127;MPI_SURUDI_127N5"
/tissue_type="whole larva"
/dev_stage="larva 2-3 weeke"
/lab_host="P.coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/note="Vector: pSportl, Site_1: NotI; Site_2: SalI; Random primed and directionally cloned in pSportl vector using a NotI (5'-pGACTAGTCTCAGATCGCGAGCGGCCCC (T)15-3' and a SalI 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Strongylocentrotus purpuratus"
mol_type="mRNA"
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291.00
54.88%
32.56%
4.88%
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KEYWORDS
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603798349F1 CSEQCHN23 Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
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Tel: 01612008930
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AGATATAGACCAAGAAGGGCTGATGATGAGATTGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simon.Hubbard@umist.ac.uk
/clone lib="CSEQCHN23"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
/note="Organ: heads; Vector: pBluescript Vas
/note: policy vas
/note: pBluescript II KS(+); Site_1:
/note: policy vas
/note: pBluescript II KS(+); Site_1:
/note: place: p
                                                                                                                                                                                                                                                                                                                                       /mol type="mRNA"
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                            dev_stage="22"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                               clone="ChEST765b13"
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cDNA clone ChEST765b13 5', mRNA
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compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91; 9228-923 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used." σ

US-10-044-692-2 (1-1132) x BU224024 (1-813) Query Match: DB: Best Local Similarity: Percent Similarity: Score: Alignment RESULT 48 BX882610 REFERENCE AUTHORS ACCESSION DEFINITION SOURCE KEYWORDS VERSION rocus ORGANISM ö 48 Scores: 418 358 189 301 173 241 153 181 133 121 113 466 199 61 236 LysArgProArgArgGlyAlaAlaPro 244 73 EST. Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss Oncorhynchus mykiss Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Euteleostai; Actinopterygii; Neopterygii; Teleostai; Euteleostai; Actinopterygii; Salmoniformes; Salmonidae; Onco BX882610.2 BX882610.2 EST. BX882610 tcbk Oncorhynchus mykiss Protacanthopterygii; Salmoniformes; Solution of the Control of the mRNA sequence. GlnValSerCysLeuLysGluLeuValAlaArgValLeuGlnArgLeuCysGluArgGly AlaLysAsnValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgGlyGlyProPro 112 GlySerGlyAlaTrpGlyLeuLeuLeuArgArgValGlyAspAspValLeuValHisLeu GTTTTGCCATCTTCGTGTATATACAGCTATCTGTCCAATACTGTAACAGAAACGATTCGC GluAlaPheThrThrSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArg CysGluArqAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAla CGACGGTACTCAAGGTTTAAACATAATAGCTTGCTTGACTATGTGCGAAAAAGGCTTGTG CAACCAATTTATGAACTT---ATTTCGCGTAACGTAGGGCCATCCCCAGGGTTTGTTAGA ProProLeuTyrGlnLeuGlyAlaAlaThrGlnAlaArgProProPro-------ĊŢĠĠŖĠĊŖĊŢĠŢĠĊŖĊŢĊŢŢĊŖŢĠĠŢŢĊĊĊĊŖŖĠŢĸĸĊŢĠĸŢĸĊĊŖĠĠŢĊŢĠĊĠĠĠ LeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGlnValCysGly ATCAGTGGCCTCTGGGAGATACTGCTGAGTAGGATAGGGACGACGTGATGATGTACCTG ProGlyAlaArgArgArgGlyGlySerAlaSerArg-----SerLeuProLeuPro ACAAAGCCTAGGTCTGGTTATCAGCCT 1.57e-09 284.50 55.03% 39.15% 4.77% AGACGTCGAGGTCGTGTCTCCAGCAGGAGAAAACAGAAGGAGCCATAGGAT GI:42815406 CACTATCTTTCCAAGTCACAGTGGTGGAAGTGCAGGCCG---HisAlaSer-----GlyProArgArgArgLeuGly Length: Matches: Conservative: Mismatches: Indels: Gaps: 543 mRNA linear EST 20-JUL-2004 cDNA clone tcbk0060c.h.01 5prim, 813 74 30 60 25 417 180 60 357 188 172 240 152 516 235 465 218 198 300

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Sequence cleaned of vector, adaptator and repetitions.
at sigenasupport@jouy.inra.fr to obtain the chromatogra
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Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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On Dec 18, 2003 this sequence version replaced gi:40127495
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                                      ACACCCAAAATGCCTGAAGACTTCAAGGCCATC 395
                                                                                                                                                                                                                                                                                          GCTTTAACAGGTAGCCTTCAGTATGAGGCAGTAGAACTGATATACTGTCTGGCCTTCCTG
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                                                                                                                                                             GlnThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAla 1119
                                                                                                                                                                                                        TIGGTICTGICCCGTCAICGCCCCCTCTACTACCAICTCCTCGCTCCGCTACGCACACGT
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                                                                           AsnProAlaLeuProSerAspPheLysThrIle 1130
                                                                                                                        AAGAGGAAGCTGGAGGGGAAGCTGGAGGGTTTGAGATTGGCCCGAATCAGACAGGCTGCC
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/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois FIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352;
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy.en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
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/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
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Seq primer: M13R.
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Sequence cleaned of vector, adaptator and repetitions. Co
at sigenasupport@jouy.inra.fr to obtain the chromatogram
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 731)
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                                                                               AlaSerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLys 1059
                                                                                                                                                             ProPheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgVallleSerAspThr 1039
                                        GCGGAGTACACCAACCATCTAGTCAGACTCTGCAACAAAGGTGTGTCTCTAGGCTGTAAG
                                                                                                                          CCGTTTGGTCAGAAAGTGGGCGGAAACCACTCGTACTTCCTCAATCTGATCTGGGACTTG
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/db_xref="taxon:8022"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N. Expressed genes in Ciona intestinalis (2004) Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BW363763 Yutaka Satou unpublished cDNA library, mature adult whole animal Ciona intestinalis cDNA clone cima830o13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 651)
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Ciona intestinalis
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Department of Zoology
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                                                                                                                                                                     HisSerSerPro---TrpGlnValTyrGlyPheValArgAlaCysLeuArgArgLeuVal 473
                                                                                                                     ProProGlyLeu---TrpGlySerArgHisAsnGluArgArgPheLeuArgAsnThrLys 492
SerValArgAspCysAlaTrpLeuArgArgSerProGlyValGlyCysValProAlaAla
                                                           LysPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnGluLeuThrTrpLysMet
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                                                                                                                                                                                             ProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPheArg :::|||||||||||||
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CATATTTACAATGGGTGGAAACAATTTGTTCTT
                                                                                                                  AGGTTGAGGAACGCCGACAAGATGGCTGACATGGTCCCCATTCGAAGTAATTGCTTCTGTG
                                                                                                                                            ArgGluLysArgAlaGluArgLeuThrSerArgVal-----LysAlaLeuPheSerVal
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                                                          TTGAAATTGGTTTGTAGTAAAGTCCCCCAAGCCACCGGGTTTGCCACACAACATCGTGCT
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Search completed: October 28, 2004, 20:46:57 Job time: 7891 secs

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Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MXX=100
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-MAXLEN=200000000 -USER=US10044692 @CGN 1 824 @runat 28102004 103657 1462
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9749728B *** *** *** *** *** *** *** *** ***	ALIGNMENTS	US-09-799-788-32 US-09-733-294A-3 US-09-933-294A-3 US-09-935-052-1 US-10-054-611-224 US-10-054-611-224 US-10-054-611-224 US-10-054-622-1 US-10-044-639-1 US-10-325-810-1 US-10-325-810-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-34 US-10-325-810-32 US-10	;
TY OF DIFFERENTIATION INTO			

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; PRIOR FILING DATE: 2000-11-02; NUMBER OF SEQ ID NOS: 80; SOFTWARE: Patentin Ver:2.0; SEQ ID NO 32; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32
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PRIOR PPLICATION NUMBER: DE 10100586.5
PRIOR PPLICATION NUMBER: DE 10155280.7
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-10-26
PRIOR PPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 3399
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
TITLE: telomerase reverse transcriptase
PATENT DOCUMENT NUMBER: AF015950
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                                                                  AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCy8HisGlnAlaPheLeuLeu
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LENGTH: 4015
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APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Edward V. Wancewicz
ITILE OF INVENTION: ANTISINSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: 1894-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 108
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NAME/KEY: CDS
LOCATION: (56)...
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ORGANISM: Homo
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GENERAL INFORMATION:

APPLICANT: Morin, Gregg B.

APPLICANT: Morin, Gregg B.

APPLICANT: Geron Corporation

TITLE OF INVENTION: Human Telomerase Catalytic Sulfile REFERENCE: 018/258c

CURRENT APPLICATION NUMBER: US/09/990,080

CURRENT FILING DATE: 1998-08-03

PRIOR APPLICATION NUMBER: US 09/052,864

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NO5: 21

SOPTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1

LENGTH: 4015
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          LENGTH: 4015
TYPE: DNA
ORGANISM: Homo :
FEATURE:
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Best Local Similarity:
Query Match:
DB:
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; OTHER INFORMATION: human telomerase US-09-990-080-1
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reverse transcriptase (hTRT)
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ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAG GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 CGGGCCTGGAACCATAGCGTCAGGGAAGGCCCGGGTCCCCCTGGGCCTGCCAGCCCCGGGT GCCACTCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA CTGGTGGCTCCCAGCTGCCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCCT LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 4015 1132 0 0 0 160 895 280 835 260 240 220 595 180 475 140 120 80 40 115 20 775 715 655 200 535 415 295 60 175 235

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01 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgP	41 76 61 36 36	481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500	GCCCCCGAGGAG 1. SerProTrpGln 4	1 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 40	GCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAJGCAGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGCACATGCTCTACTCCTCAGGCGACAAGCACAAGCACATGCCAGCTGACTGA	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
Oy 961 ASRATGLYPHELYSHALGOLYALGASHICLALGASHICLALGA	275 CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGCCTTGGTGGCACGGCTTTTGTT 275 CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 1	2576 CTCTG 861 GlyLe 861 GlyLe 2636 GGGCT 881 LysTh 2696 AAAAA	Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820		701 AspPrc	Qy 661 LeuPheSerValleuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680

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RESULT 5
US-09-843-676-224
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Patent No. US20020164786A1
GENERAL INFORMATION:
                                                INFORMATION FOR SEQ ID NO: 224:
                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION UNBER: US/99/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION NUMBER: US/98/854,050
FILING DATE: 09-WAX-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
ATTONEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0300
NEORMATION: FOR SERO ID NO. 224.
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCES: 225
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
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                               SEQUENCE
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STATE: California
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                NCE CHARACTERISTICS:
LENGTH: 4015 base pairs
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LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly
                                                                                                                                                                                                                                                                  LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla
                                                                  AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg
                                                                                                               CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT
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RESULT 6
US-09-953-052-1
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Patent No. US20020173476A1
GENERAL INFORMATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919

FILING DATE: «Unknown»

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                          ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                   APPLICATION NUMBER: US/09/953,052 FILING DATE: 14-Sep-2001 CLASSIFICATION: <Unknown>
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INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                 Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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FEATURE:
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LOCATION: 56..3454
OTHER INFORMATION: /
transcriptase (hTRT)
  SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu
                                                               TTCGCGCTGCTGGACGGGCCCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGC
                                                                                    PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE: 14-AUG-1997
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
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Matches:
Conservative:
Mismatches:
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RESULT 7
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
Andrews, William H.
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                                                          Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Best Local Similarity:
Query Match:
DB:
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; OTHER INFORMATION: /product= "hTRT"
; /note= "human telomerase reverse
transcriptase (hTRT) catalytic protei
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
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INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
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APPLICATION UNMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: '536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
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                                                                           GIGCIGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGCAG
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STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
       AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 8
US-10-208-243-1
(Sequence 1, Application US/10208243; Sequence 1, Application US/10208243; Publication No. US20030044394A1; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
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                                                                                                                                                                                GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe
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                                                                                                                                  SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly
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# TITLE OF INVENTION: Methods and Compositions for Eliciting an I
# TITLE OF INVENTION: Response to a Telomerase Antigen
# FILE REFERENCE: 015389-003500PC
# CURRENT EPPLICATION NUMBER: US/009/675,321
# PRIOR APPLICATION NUMBER: US/09/675,321
# PRIOR FILING DATE: 2000-09-28
# PRIOR FILING DATE: 2000-09-28
# PRIOR APPLICATION NUMBER: US 60/112,006
# PRIOR APPLICATION NUMBER: US 60/112,006
# PRIOR APPLICATION NUMBER: US 60/112,006
# PRIOR APPLICATION NUMBER: US 60/12,006
# PRIOR PILING DATE: 1999-03-31
# PRIOR PILING DATE: 1999-03-30
# NUMBER OF SEQ ID NOS: 2
# SOFTWARE: Patentin Ver. 2.0
# SEQ ID NO 1
# LENGTH: 4015
# TYPE: DNA
# ORGANISM: Homo sapiens
# FEATURE:
# NAME/KEY: CDS
# LOCATION: (56)...(3454)
# OTHER INFORMATION: human telomerase reverse transcriptase ('US-10-208-243-1)
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      CTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCTGCGCGCTCTTTGTG
                                                                                                              LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
                                                                                                                                               ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly
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Conservative:
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RESULT 9
US-10-054-295-224
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Publication No. US20030044953A1
GENERAL INFORMATION:
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                          NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
CORRESPONDENCE TOwnsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                          Nakamura, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
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                                                                              Version #1.30
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMÉ: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-196
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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LeuArgArgValG1yAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
                                                                                                                                                                                                                                                                                                              AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu
                                                                                  SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140
                                                                                                                                     TTCGCGCTGCTGGACGGGGCCCGGGGGGCCCCCGAGGCCTTCACCAGCGTGCGC
                                                                                                                                                               PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
                                                                                                                                                                                                                                  ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
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                                                            AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTTGCTG
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Matches:
Conservative:
Mismatches:
Indels:
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당 양 문

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461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 436 GTGTACGGCTTCGTGCGGCCTGCCTGCGCCTGGTGCCCCAGGCCTCTGGGGCTCC 1495 436 ArgHisAsmGluArgArgPheLeuArgAsmThrLysLysPheIleSerLeuGlyLysHis 500 481 ArgHisAsmGluArgArgPheLeuArgAsmThrLysLysPheIleSerLeuGlyLysHis 500 496 AGGCACAACGAACGCCCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT 1555 496 AGGCACAACGAACGCCCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGACAT 1555 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520 556 GCCAAGCTCTCGCTGCAGGAGCTGACGTGAAGATGAGCGTGCGGAAGATGAGCTGCGCTTGGCTG 1615	1315		1			CGGT 715 Qy 581	AlaProSerCysAlaTyrGInValCysGyProProLeuTyrGInLeuGlyAla 180	76 CTGCGCCGCGTGGGCGACGACGACGTGCTTCACCTGCTGGCACGCTGCTGCGCGCTCTTTGTG 535 C1 TONTOL N = TO
rgGlyLysSerTyrValGinCysGlnGlyTleProGlnGlySerTleLeuSerThrLeu [1]	InGluThrSerProLeuArgAspAlaValIValIIeGluGlnSerSerSerLeuAsnGl	CCCAGGACAGGCTCACGGAGGTCATCACCAGCAGCATCATCAACCCCAGAACACGTACTGCCAGCAGCACCAGAACACGTACTGCCAGCAGCACCAGAACACGTACTGCCAGAACACGTACTGCCAGAACACGTACTGCCAGAACACGTACTGCCAAGGCCTTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCAAGGCCTCCACCTGACCAGCCCTCCAGCCCTACATGCGACAGTTCCGTGGCTACCTGACCAGACCTCCAGCCCGTACATGCGACAGTTCCGTGGCTCACCTGACCAGACCTCCAGCCCGTACATGCGACAGTTCCGTGGCTCACCTGACCTTGACCAGACCTCCAGCCCGTACATGCGACAGTTCCGTGGCTCACCTGACCTTGACCTTGACCAGACCTCCAGCCCGTACATCCAGCCACAGTTCCGTGGCTCACCTGACCTTGACCTTGACCTTGACCAGCCCGTACATCCAGCCACAGTTCCGTGGCTCACCTGACCTTGACCATGCCAACATCCAACCATGCCACAGTTCCGTGGCTCACCTGACCATGCCAACATTCCGTACATGCCACAGTTCCACCTGACCATGCCACCTGACCTGACCATGCCACCAGCCCTTACCTGACAGACCTCCACCTGACCAGACCTCCACCTGACCAGCCCTACACATCCAACAACACCTGACAACACCTGACCAACAACACCAACAACACAACAACAACAACAACAACA	CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCCGTGTCGGGCCCAG AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA LeuPheSerValLeuAsmTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 	CTGTCGGAAGCAGAGCTCAGGCAGCATCGGGAAGCCAGGCCCCGCCCTGCTGACGTCCAGA LeuArgPheIleProLy8ProAspGlyLeuArgProIleValAsnMetAspTyrValVal	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluTrpSerLysLeuGlnSerIleGlyIleArgGluIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGGACACCGTCTGCGTGAGAGAT PALALLYS PheLeuHiSTrpLeuMetSerValTyrValValGluLeuLeuArgSerPh	gArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIl

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RESULT 10
US-10-054-611-224
; Sequence 224, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
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                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el
NUMBER OF SEQUENCES: 225
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                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY,AGENT INFORMATION:
NAME: APPLE, MANDER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcriptase (hTRT) catalytic protein component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
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{\tt PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg}
                                                           ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
                                                                                                           AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu
                                                                                                                                                                               CGCGGGGACCCGGCGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
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Matches:
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461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480 	441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460 	421 ProAlaAlaGlyValCysAlaArgGluLysBroGlnGlySerValAlaAlaProGluGlu 440 		ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro		CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 3	ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgBroTrpAspThrPro 32	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 28	GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	א אי	01 ArgalaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 22	81 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 2	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 	141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160 	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140 	356 TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGC 415
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Sequence 1, Application US/10105963
Publication No. US20030068818A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst
TITLE OF INVENTION: Recombination
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             System
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SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: (56)...(3454)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/277,811
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 40
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 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg
                                                                                              AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu
                                                                                                                            LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
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                                                ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly
                                                                                  GCCACTCAGGCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA
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Matches:
Conservative:
Mismatches:
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A B C	8 B 8 B 8
	601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

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RESULT 12
US-10-044-692-1
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                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELLOMERASE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <UNKnown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
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CITY: San Francisco
STATE: California
COUNTRY: United States of America
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Center, 8th Floor
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FILING DATE: 25-APR.1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR.1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT.1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION POR SEQ ID NO: 1:
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LOCATION: 56.3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protei
component"
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TYPE: nucleic acid
STRANDEDNESS: single
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Conservative:
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Db 11.16 CHICAGASACCAGASTROCCUSTORIC COCCAGAGACCACTURA CONTROCCUSTORIC CONTROC	201 ArablatpaseitisGerrialArgGiublackyAlbroteacidyMenbroallaProdit 220	161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
	1736 TITTAN 581 TrySe; 601 LeuSe; 601 LeuSe; 601 LeuAr; 1856 CTGTC; 621 LeuAr; 1916 CTGTC; 621 LeuAr; 1916 CTGTC; 621 LeuPh 1976 GGAGC; 631 LeuPh 2036 CTGTT; 681 LeuCh 2036 CTGTT; 701 AspPr 701 AspPr 701 ProG1 2156 GACC; 721 ProG1 2156 GACC; 721 ProG1 2176 GACC; 721 ProG1 2276 CTGGG; 761 SerHi 2336 AGCC; 781 GlnGl 2336 AGCC; 821 ALSG 2456 GCCAG; 821 ALSG 2576 CTCTC 2576 CTCTC 2576 CTCTC 2576 GGGGC; 2576 GGGGC; 2576 GGGGC; 2576 GGGGC; 2576 GGGGGC; 2576 GGGGGC; 2576 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1616 CGCAGG 541 Leuhla 1676 CTGGCC

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RESULT 13
US-10-044-539-1
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                                                        NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
COMMENCE ADDRESSE: Townsend and Townsend and Townsend and Townsendero Contry: San Francisco
STATE: California
                                                                                                                                                                       Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUWAN TELOMERASE CATALYTIC SUBUNIT:
THERAPEUTIC METHODS
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      COMPUTER READABLE FORM
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                        COUNTRY: United States of America ZIP: 94111
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Center, 8th Floor
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-044-539-1
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/861,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1996
APPLICATION NUMBER: US 08/724,643
FILING DATE: 101-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPle, Randolph T
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
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LOCATION: 56..3454
OTHER INFORMATION: /product= "hTR
/note= "human telomerase reverse
transcriptase (hTRT) catalytic prot
component"
                                                                                                                                                                                                                                                                                           ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly
                                                                                  AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
                                                                                                                                        CGCGGGGACCCGGCGCTTTCCGCGCGCGCTGGTGCCCAGTGCCTTGGTGTGCCCTGG
                                                                                                                                                               ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 435
RAPPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatil
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Matches:
Conservative:
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Indels:
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ol GINGIUINISELELUS CHARGAS DALA VALVAS CALLES CONSTITUENTE DE LOCUMBRICA CON CONTROL	40 375	421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 4
61 SerHi 36 AGCCA	20	6 P
41 ValAr 76 GTGCG	255	381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 4
	80	
01 AspPi 56 GACCC	60	341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 3
	340 Db	321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 3
	20	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 3
41 76	00 Db	1 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 3
21 16	и о	ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu
	и о	1 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly
96	240 Db	
36	220 Db	201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 2
The Lean I	200 Db	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 2
16 CGCAG	.80 Db	161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 1
56 GCCAA	35 Db	141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 1
AGGCA	140 Db 475 Ov	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 1
36 GTGTA	120 Db	101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 1
461 ValTvrGlvDheValArgAlaCvsLeuArgArgLeuValProDroGlvLeuTrpGlvSei	55	296 GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGC 3

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; Sequence 1, Application US/10325810; Publication No. US20030204069A1; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.; Lingner, Joachim; Nakamura, Toru; Nakamura, Toru; Chapman, Karen B.
                                                                                                                                      RESULT 14
US-10-325-810-1
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                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                Score:
                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID US-10-325-810-1
                                                                                                   Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
PRIOR APPLICATION CONTROL OF THE PRIOR APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/843,050
FILING DATE: 06-MAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/854,050
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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ADDRESSEE: Townsend and
STREET: Two Embarcadero
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                              LOCATION: 56..3454
OTHER IMPORMATION: /product= "h'
note= "human telomerase reverse
transcriptase (hTRT) catalytic pi
component"
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Andrews, William H.
OF INVENTION: Human Telomerase Catalytic Subunit
R OF SEQUENCES: 633
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                                       Length:
Matches:
Conservative:
Mismatches:
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  Gaps:
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341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360 	321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340 	301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320 	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300 	261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280 	241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260 	ArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgPı 	201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220 	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu 200 	161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180 	141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160 	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140	101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120	81 ValalaargValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100 	61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCYsLeuLysGluLeu 80 	41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60	21 ValleuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40 	1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20	044-692-2 (1-1132) x US-10-325-810-1 (1-4015)
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701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720			GlyAlaArgThrPheArgArgGlulysargAlaGluArgLeuThrSerArgVallysAla 6				561 PheTyrValThrGluThrThrPhe6lnLysAsnArgLeubhePheTyrArgLysSerVal 580	41 HEMALALYSERELEUHISTT DLEUWECSER VALTYYVALVALGILULEULEUARGSER PHE 5	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	AlalysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 5	ArgHiaAsnGluArgArgPheLeuArgAsnThriysLysPheIleSerLeuGlyLysHis 5	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 4	GluaspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 4				ValGLUTARI LepheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	76 CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC 1

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             AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
                                                                      SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly
                                                                                                              PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla
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PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120

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APPLICANT: Geron Corporation
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Gold D.
APPLICANT: Joseph, Gold D.
APPLICANT: John, Irving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Mok, Michael
APPLICANT: Mok, Michael
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Dov
TITLE OF INVENTION: Embryonic Stem Cells
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Custom
SEQ ID NO 1
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Query Match:
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TYPE: DNA
ORGANISM: Homo sapi
FEATURE:
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OTHER INFORMATION:
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841 LeucysSerieuCysTyrGlyAspNetGluAsnivsLeuDheAlaGlyIleArgArgAsp 860 1576 CTCTCCACCTGTGTACGCGGCACATGGAGAACAGCGTGTTTTCCGGGGGATTCCGGGGGAC 2635 861 GlyLeuLeuLeuArgLeuValAspAspBrbLeuLeuValThrProHisLeuThrHisAla 860 862 GGCTGTCCTCGGTTTGTGTGATGATTTCTTTTGTGTGTACACCTCCCCCACCGG 2695 861 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsmLeu 900 16	υμ	3 1	ω μ	3 1	3 1	ω μ	ω μ	N	N	2	8	N	N	N	N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides cells originating in the human bone more umbilical blood cells which are capable of differentiating into cardiomyocytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, the study of cardiomyocyte differentiation. The present sequence is oligonucleotide described in the exemplification of the invention
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The present invention describes cells originating in bone marrow or umbilical blood cells which are capable of differentiating into cardiomyocytes. Also described are: (1) cardiomyocytes produced by th differentiation of the cells; (2) a method for carrying out the differentiation into cardiomyocytes, regulated by a promotional and/o inhibitory factor; (3) a method for the differentiation of the cells cell types other than cardiomyocytes; (4) drug compositions promoting

and/or by the

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Disclosure;

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                                                                                             Cells capable of differentiating into cardiomyocytes and originating bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells; especially antibodies which recognise on the cells; (6) a method for screening factors which promote the proliferation of the cells; (7) a method for immortalising the cells by expressing telomerase in them; (8) drug compositions for the treatment of heart disease which contain the immortalised cells; and (9) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomyocytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomyocyte differentiation. ANH44351 to ANH44409 and ANB99915 to ANB99935 represent sequences used in the exemplification of the present invention
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New HIV-1 Reverse Transcriptase and human Telomerase Reverse Transcriptase proteins and nucleic acids, useful in gene therapy or for treating or preventing unregulated cellular growth, e.g. cancer cell or

tumor growth.

Example 1; SEQ ID NO

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HIV-1; reverse transcriptase; human telomerase reverse transcriptase;
hTERT; chimeric; catalytic site; unregulated cellular growth; cancer;
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                                                                                  Inhibiting expression of target gene, useful oncogenes, by administering double-stranded target and having an overhang.
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26-CCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; gene; ds.
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25-26; 100pp; German.

Inhibiting expression of t by introducing into cells to the target.

target genes, useful s two double-stranded

e.g. RNAs

for treating tumors, that are complementary

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide

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Alignment Pred. No.: 666666666666888 중 유 5 Ś Query Match: DB: S Ş 뫄 Ş Ş δ 멍 δ DЬ Ś 밁 8 망 Ś B В Ś В US-10-044-692-2 (1-1132) x ABZ35720 (1-3399) Percent Similarity: Best Local Similarity: 밁 밁 밁 pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other; No.: 141 221 601 201 541 181 481 161 421 361 121 301 TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGC 101 241 121 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 13 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln _ GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla CTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTG SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGC CGCGGGGACCCGGCGCTTTTCCGCGCGCGCTGGTGCCCAGTGCCTGGTGTGCCTTGG GTGCTGCCGCTGGCGACGTTCGTGCGGCGCCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAG ATGCCGCGCCCCCCCCCCGCAGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCGCGAG MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu GCGAGGAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCCGATGCCCAAGAGGCCCAGGCGT CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT GCCACTCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA 2.38e-218 5961.00 100.00% 100.00% Length: Matches: Gaps: Conservative: Mismatches: Indels: 3399 1132 0 0 0 180 260 240 660 600 200 160 420 140 360 300 100 240 80 60 120 40 60 720 220 540 480 180

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This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with

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Disclosure; Page 30-31; 98pp; German.

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                                                          Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon.
                                                                                                                                                                                                              Oligoribonucleotide; interferon; prion; inhibition; human; ds.
                                                                                                                                                  09-JAN-2001; 2001DE-01000587.
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                                                             ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn
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ABL91685;

28-MAY-2002

Human polynucleotide SEQ ID ŏ 28

Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.

DE10100586-C1.

11-APR-2002

09-JAN-2001; 2001DE-01000586

2001DE-01000586

(RIBO-) RIBOPHARMA AG

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중 음 중 음

중 음 중

Inhibiting gene expression: introducing double-stranded terminal bases. in cells, useful for e.g. treating tumors, complementary oligoRNA having unpaired ş

13; Page 27-28; 104pp; German.

RESULT 8
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ID ABL9
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XX ITA The invention relates to a method for inhibiting expression of a target gene (ABL9158-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-

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                                                                                                          Eliciting an immune response in a mammal specific for its own telomerase reverse transcriptase (TERT), useful for treating or preventing cancer, comprises administering a composition containing TERT of another
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                                          Disclosure; SEQ ID NO 1;
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ACTCAGGCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA AlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 22 		428 AGCIACCIGCCAAACACGGIGACCAACACGAAGAAAAAAAA	368 TTCGCGCTGCTGGACGAGGCCCCGCGAGGCCTTCACCACCACCACGAGGCCTTCACCACCACCACGAGGCCTTCACCACCACGAGGCCTTCACCACCACGAGGCCTTCACCACGAGGCCTTCACCACGAGGCCTTCACCACGAGGCCTTCACCACGAGGCCTCACGAGGCCTGAGGCCTGAGGCAGGC	1 ValAlaArgVali 8 GTGGCCCGAGTGO	188 CGCGGGAACCCGGCGCTTTCCGCGCGCGCGGGGGCCCAGTGCCTGGGGGGGG		-10-044-b92-z (1-1132) A FARZ 100 (2 1770) 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArg	pred. No.: 2.63e-218 Length: 3798 Score: 5961.00 Matches: 1132 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 100.00% Indels: 0 DB: 2 Gaps: 0	(Updated on 25-MAR-2003 to correct PR field.) Sequence 3798 BP; 613 A; 1311 C; 1212 G; 662 T; 0	CC therapputically as inhibitors. Nucleic actual requests and contemplated CC diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated CC are transgenic animals in which the TP2 gene has been inactivated or is CC overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or CC they are delivered from engineered cells or gene therapy vectors.	CC activity, e.g. for treatment of cancer. Its polypeptimes win and concern to screen for agents that inhibit TP2 activity or its binding to TRIP1 CC (see AAW61347) or telomerase RNA, potentially useful therapeutically, CC also to raise specific antibodies useful in immunoassays and CC also to raise specific antibodies useful in immunoassays and concern to the con	CC LIM1803 CDMA. EXPRESSING FA General Control of CC telomerase activity and thus proliferation for treatment of e.g. HIV CC infection, AIDS and ageing disorders, while expressing an inactive mutant CC of TP2 (or molecule antisense to the gene) is used to decrease telomerase CC of TP2 (or molecule antisense to the gene) is used to decrease telomerase	CC This full-length character to the telemerase complex. The sequence CC see AAW61350), a novel protein of the telemerase complex. The sequence CC was deduced from overlapping partial clones #32 (see AAV27872) and TP2-15 CC (see AAV27875), which were obtained from a human colon tumour cell line CC (see AAV27875).	c.,
Qy 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580		501 AlaLysLeuSerLeuGInGlüLeuThriphysmelservalatiyaspyssisiilillillillillillillillillillillill	Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500	441 UNAB HILABET DATA SHORT OF THE CONTROL OF THE C	421 1328	0—H	Qy 361 ValGluThrIlePheLeuGlySerArgFroIrDWcLFLOGIALLIA (1977) Option		301 968	281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 	261 848	~1 N	221 728	Db 668 CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCC

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AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle
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                      ArgiysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal
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09-MAY-1997;
14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews
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standard; DNA; 4015 ΒP

CT-1999 (first entry)

nn telomerase catalytic domain DNA.

ζ omerase; catalytic domain; human; quantitation; tumour cell; melanoma; y fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia; te lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer; ast cancer; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for the quantitation of tumour cells in a body fluid which comprises (1) enrichment or isolation of tumour cells in the sample, (2) amplification of mRNA from these cells that encodes the catalytic subunit of telomerase and (3) quantifying the amount of amplified mRNA. The method is applied to tumour cells derived from (micro)metastases, e.g. associated with a wide range of tumours such as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or breast etc. This sequence encodes a human telomerase protein catalytic domain
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reverse transcriptase (hTRT) 17-JAN-2000

(first

entry)

transcriptase; human; hTRT; cell proliferation;

sapiens

Location/Qualifiers 56. .3454 /*tag= a

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cDNA; ВÞ

AAZ30154;

26-JAN-2000 (first entry)

cDNA encoding a human telomerase reverse transcriptase (TRT)

RESULT 14
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ID AAZ30
XX AAZ30
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Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological destruction; telomerase; cancer; proliferation disease;

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A CONTROLLE CONT	Qy 821 ArgGlyLysSerTy: Db 2516 AGGGGAAGTCCTAG Qy 841 LeuCysSerLeuCys	Qy 801 AlaSerSerGlyLeuPheAsp 	Qy 781 GlnGluThrSerPro	Qy 761 SerHisValSerThi 	Qy 741 ValArgArgTyrAla 	000 	Qy 701 ASPPROPROPROGIU 	Qy 681 LeuGlyLeuAspAs; Db 2096 CTGGGCCTGGACGAT	Oy 661 LeuPheSerValLev	Oy 641 GlyAlaArgThrPhe	Qy 621 LeuArgPheIlePro	Oy 601 LeuSerGluAlaGlu	Qy 581 TrpSerLysLeuGlr Db 1796 TGGAGCAAGTTGCAA	Qy 561 PheTyrValThrGlt	Qy 541 LeuAlaLysPheLeu	1616 CGCAGGAGC	1556 GCCAAC	Qy 501 AlaLysLeuSerLeu
1555 1615 1615 1615 1615 1616 1676 1677 1677 1677 1887 1988 1999 1001 1001 100 100	nGlySe	ValPheLeuArgPheMetCysHisHisA STCTTCCTACGCTTCATGTGCCACCACG		SValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVe	.ValValGlnLysAlaAlaHisGlyHisValArgL; 	pArgLeuThrGluValIleAlaSerIleIleLysProGlnAs 	iLeuTyrPheValLysValAspValThrGlyAlaT)IleHisArgAlaTrpArgThrPheValLeuArgV. 	PheServalLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGl 	ArgArgGluLysArgAlaGluArgLeuThrSerA:)LysProAspGlyLeuArgProIleValAsnMetAi	WalargGlnHisArgGluAlaArgProAlaLeuLe 	"sLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValG] 	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrAi 	HisTrpLeuMetSerValTyrValValGluLeuL 		CAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTK	GlnGlubeuThrTrpLysMetSerValArgAspC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quantitating expression of mRNA encoding hTERT, the catalytic subunit of telomerase, as an indicator of cancer, by amplifying RNA using primers complementary to hTERT gene sequence and quantitating amplified products
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           LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal
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861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880	2516 AGGGCAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCCCACGCTG 2575 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgAsp 860	801 AlaSerSerGlyLeuDheAspValEneLeuArgPheMetCYsH1sH1sAlaValArg11e 820	GlnGluThrSerProLeuArgAspAlaVallaGluGlnSerSerSerLeuAsnGlu 8	1 Ser	741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760 	721 ProGlnAspArgLeuThrGluVallleAlaSerIleIleLysProGlnAsnThrTyrCys 740 	701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720 	681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700 	661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680	641 GlyalaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660 	621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640	601 LeuSerGluAlaGluValArgGlnHi8ArgGluAlaArgProAlaLeuLeuThrSerArg 620	581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600 	561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580 	541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560 	521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540

1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132	1101 ThrGinLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120	1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100	1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080	1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060	1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgVallleSerAspThrAla 1040	1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020	981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000	961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980	941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960	921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940	901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920	

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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                         Direct Submission
Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
This sequence was made by sequencing genother based on alignment.
                                                                                                                                                                                                                             Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Science 302 (5652), 1960-1963 (2003)
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                                                                                    /gene="TERT"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1584)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. AY407350
Pan troglodytes TERT gene, VIRTUAL genomic survey sequence.
AY407350
AY407350.1 GI:39763321 2 (bases 1 to 1584) Clark, A.G., Glanowski, S., gene trios Science 302 Pan troglodytes (chimpanzee)
Pan troglodytes 14671302 Inferring nonneutral (5652), 1960-1963 evolution Nielson, R., (2003) from DNA linear GSS 15-DEC-2 TRANSCRIPT, partial sequence, human-chimp-mouse Kejariwal, A., GSS 15-DEC-2003 orthologous

Thomas, P.,

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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order: them based on alignment.
Location/Qualifiers
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                        CCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCC 2408
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                                                                     CCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTA 2348
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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RESULT 3 AY407351 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1835)
1 (bases 1 to 1835)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., AY407351.1 GI:39763322 GSS.
Mus musculus (house mouse) AY407351 Mus musculus TERT gene, genomic survey sequence ĀY407351 1835 bp , VIRTUAL DNA linear GSS 15-DEC-2003 TRANSCRIPT, partial sequence,

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Direct Submission
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Inferring nonneutral evolution from human-chimp-mouse orthologous
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1 (bases 1 to 925)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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BM453198
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Plate: LLAM12208 row: p column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                     CACCATCCCCCAGGACAGGCTCACGGAGGTCATCATCAAACCCCCAGAACAC
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                                                                                                                                                                                                      GTACTGCGTGCGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGC
                                                                                                                                                                                                                                                 GTACTGCGTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGC
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  TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT
                             TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT
                                                                                                                                              CTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC
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Location/Qualifiers
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:5529840"
/tissue_type="leiomyosarcoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/clone_lib="NIH_MGC_71"
/clone_solub="NHH_MGC_71"
/clone_solub
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Pred. No. 1.7e-157;
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                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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UI-M-F10-byx-f-12-0-UI.r1 NIH BMAP FI0 N
IMAGE:6400523 5', mRNA sequence.
BU702370
BU702370.1 GI:23627105
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                               This clone was contributed by the Brain Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCT
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                                                                                                                                                                           primer: pYX-5
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6400523"
                                                                                                /organism="Mus musculus"
                                                                                                                                                   ocation/Qualifiers
                                                                                                                              . 851
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; Murinae; Mus
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CDNA clone
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Matches 638;
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                                                                                                                                   TGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCA 2915
                                                                                                                                                                                                                                                                                                                                      CGCCTCACTTGGACCAAGCAAAAAACCTTCCTCAGCACCCTGGTCCATGGCGTTCCTGAGT
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                                           TCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAAC
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TTAAGACGAGCCTCACCTTCCAGAGTGTCTTCANAGCTGGGAAGACCATGCGGAACANGC
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/dev_stage="embryo 12.5dpc"
/lab host="NH108 (T1 phage resistant)"
/clome_lib="NIH_BMAP_FIO"
/clome_lib="NIH_BMAP_FIO"
/site_2: Not I; The library was constructed according site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA, synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mENA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Pred. No. 1.2e-93;
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xv57e03.xl NCI_CGAP_Lu28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Eh.D. Libeary Preparation: Life
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
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Location/Qualifiers
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/lab host="DH10B"
/clone lib="NCI CGAP Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies."
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/mol_type="mRNA"
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/clone="IMAGE:2817244"
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sapiens cDNA clone IMAGE:2817244 3',
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1 (bases 1 to 492)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
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BM824748
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K-EST0096335 S22SNU16n1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
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Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kim YS
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Location/Qualifiers
          Conservative
                                                                                                 /note=Torgan: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares M.B. (1996). Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                                                /cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-99-E07"
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11.1%; >-
100.0%; Pr
0;
      Score 445; DB 4;
Pred. No. 3.7e-82;
0; Mismatches 0;
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                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM10903 row: k column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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BG917907.1 GI:14298383
EST.
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62820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
                                                                                                                                                                                                                     High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
                      /organism="Mus musculus"
/mol type="mRNA"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:4949887"
/clone="IMAGE:494987"
/sex="female, virgin"
/tissue_type="infiltrating dd/dev_stage="5 months"
/lab_host="BH108"
        clone_lib="NCI_CGAP_Mam6"
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Murinae; Mus.

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RESULT 9
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416 bp mRNA linear EST 03-JAN-2000
xr10b12.xl NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
mRNA sequence
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Pred. No. 1.1e-76;
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Clone distribution: NCI-CGAP clone distribution
Clone distribution: MCI-CGAP clone distribution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Mammalia; Eutheria;
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TTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGA 4009
                                                                                                              AGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAA 3953
                                                                                                                                                                                                  ACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAA 3893
                                                                                                                                                                                                                                                                                     TCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCC 3833
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1:
Site_2: Noti; Cloned unidirectionally. Primer: '
Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
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/lab_host="DH10B"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zt08g02.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2187 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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                                                                                                                                                                                                                                                      GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTTCTTT
                                                                                                                                                      AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGAGGGTGCAGCTGCGGGAGCTG
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                                                                                          AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGGTGCAGCTGCGGGACGTG
                     GCCAGAACGTTCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 2038
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                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 8.3e-70;
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Contact: Brandenberger R
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Fax: 650 473 7760
Email: rbrandenbergerægeron.com
Insert Length: 409 Std Error: 0.00.
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1 (bases 1 to 409)
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GCTGCTGGACGGGGCCCCGCGGG 383
                                                                     CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360
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/clone lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tlssue_type="embryonic stem cells, cell lines
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Pred. No. 7e-6
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088 bp mRNA linear
UI-M-FY0-cgp-m-21-0-UI.rl NIH_BMAP_FY0 Mus musculus
IMAGE:30355988 5', mRNA sequence.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              gel. First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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/tissue_type="whole brain"
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/lab_nost="DH10B (T1 phage resistant)"
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/clone lib="NIH BMAP_FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 649)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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Contact: Robert Strausberg,
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     /clone="IMAGE:3035746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5.14.5,16.5,17.5dpc"
/dev_stage="embryo 13.5.14.5,16.5,17.5dpc"
/lab host="DH10B (II phage resistant)"
/clone_lib="NHIBMAP_FYO"
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/note="Organ: Brain; Vector: pyx- Asc; Site_1: BcoR I;
/note="Organ: pyx- Asc; Site_1: BcoR I;
/note="Organ: Brain; Vector: pyx- Asc; 
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/mol_type="mRNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 599)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  program coordinator."
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Pred. No. 2.7e-60;
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120

Query Match Best Local S Matches 403

Local Similarity 403;

8.0**%**; 74.9**%**;

Score 322; DB 2; Pred. No. 1.9e-56; 0; Mismatches 135

Length Indels

Gaps

0

Conservative

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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of monredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer based methods for the mouse full-length cDNA
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                   /clome lib="RIKEN full-length enriched, 8 days embryo"/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                Sequencing Center (MADO)
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: J. Baker (Stanford University)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ258274.1 GI:20459030
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XL1-Blue"
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|mol_type="mRNA"
                                                                                   'db_xref="taxon:10090"
'clone="IMAGE:5409222"
                                                                                                                                         strain="CD-1"
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ACCESSION VERSION KEYWORDS

AA811084 AA811084.1 EST.

GI:2880695

SOURCE

ORGANISM

Homo

Homo sapiens (human)

Eukaryota;

Metazoa; Chordata;

Craniata; Vertebrata;

Euteleostom1;

RESULT 16 AA811084/c

DEFINITION FOCUS

oa85c05.s1 NCI_CGAP_GCB1

340 k Homo

bp mRN o sapiens

linear

r EST 19-FEB-1998 IMAGE:1319048 3',

mRNA CDNA

mRNA sequence AA811084 S

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                      CAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGC 1808
                                                                                              GTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACCGGAGACCCACGTTTCAAAAGAA 1767
                                                                                                                                                                           CGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCTGATGAGTGT 1707
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milarity 68.3%;
Conservative
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/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
made by oligo-dT priming. DTrectionally cloned into
salI/NotI sites using the following 5' adaptor:
5'-TCGACCCACGGTCCG-3', Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
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Pred. No. 1.4e-55;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allm. Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: Greg Lennon, Ph.
                   GAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
                                                                                       CACCTGGATGGGGGTCCCTGTGGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACT
                                                                                                                                                           TGGGAGCTCTGGGAATTTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCCTG 3924
                                                                                                                                                                                                                                                                                                           CCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCT
                                                                                                                                                                                                                                                                                                                                                                               TCACTTCCCCACAGGCTGGCGCTCCGCCCCCAGGCCAGCTTTTCCTCACCAGGAG
GAATATATGAGTTTTCAGTTTTGAAAAAA 12
                                                                    TGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTG
                                                                                                                                                                                                        CGCCCTGCCCTCCTTTGCCTTCCACCCCAACCATCCAGGTGGAGACCCTGAGAAGGACCC
                                                                                                                                                                                                                                       CGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCCTGAGAAGGACCC 3864
                                                                                                                                                                                                                                                                                                                                             TCACTTCCCCACAGG-TGGCGCTCGGCTCCACCCCAGGCCCAGCTTTTCCTCACCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Pharmacia),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1319048"
/tissue_type="germinal center B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Double-stranded cDNA was ligated to Eco RI adaptors harmacia), digested with Not I and cloned into the Not I
                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 305.4; DB 1;
Pred. No. 5e-53;
0; Mismatches 1;
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Inohkawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA
clone C330020G14 5', mRNA sequence.
BB651920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 614)
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/clone lib="RIKEN full-length enriched, ES cells" note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /cell_type="ES cells"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="C330020G14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .614
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RESULT 18
AA748707/c
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Best Local Similarity
Matches 378; Conser
                                                                                                                     AUTHORS
TITLE
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                                                                                                                                                                                                                                                         ny02e05.sl NCI_CGAP_GCB1
mRNA sequence.
AA748707
                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 315)
            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., l
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                               AA748707.1 GI:2788665
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Bonaldo,
                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                       Unpublished (1997)
                                                                                                        Tumor Gene Index
                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Primates;
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Pred. No. 6.2e-50;
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                                              David Allman,
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COMMENT

cDNA Library Arrayed by: Greg Lennon,

REFERENCE

SOURCE KEYWORDS VERSION Ş 밁 Ś 밁 Ś 뫄 Ś 밁 Ş

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Location/Qualifiers
                                                                             mRNA sequence.
BE371943
BE371943.1 GI:9317215
                                                                                                               BE371943 866 r
601217728F1 NCI_CGAP_Lu29 Mus
Mammalia; Eutheria;
1 (bases 1 to 866)
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                   Mus musculus
                                                                                                                                                                                                                                                                  CTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCTCCGCCTCCACCCCAGGCCCAGCTTTTCCTCACCAGGAGCCCCGGCTTCCACTCCCCA
                                                                                                                                                                                                                                                                                                                                                          GGGCCGGGGCCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATT
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                                                  musculus (house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1270592"
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                                                  mouse)
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Pred. No. 1.2e
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                                                                                                                      musculus
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BE396925
601290610F1 NIH_MGC_8 Homo sapiens
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: LLAM8748 row: h column: 07
High quality sequence stop: 639.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                             TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGAACTTGCGGAAGACAG
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                                                                                                                                                                                                    CTCACTGCCTGTTTCCCTGGTGGTGGTTGCTGCTGGACACTCAGACTTTGGAGGTGTTCT 421
                                                                                                                                                                                                                                   CCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA 2885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
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/strain="CZECH II"
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Pred. No. 6.1e-45;
0; Mismatches 110;
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                           mRNA linear EST 21-JUL-2000 cDNA clone IMAGE:3621050 5',
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AUTHORS
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BE396925.1 GI:9342290
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM294 row: c column: 03
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                        TCATCCCCAAGCCTGACGGGCTGCGGC 1949
                                                                                                                                                                                                                                                                                                                      CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT 1805
                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT
                                                                                                                                 GCAGAGGTCAGGCAGCATCGGG--AAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCT 1922
                                                                                                                                                                                    TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTAGTCGGAA
                                                                                                                                                                                                                              TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT-GTCGGAA 1864
                                                                                                                                                                                                                                                                                 CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
TTCATCCCAAAGCTGAAGGGCTGCGGC 695
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3621050"
/tlissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 8"
/clone_lib="NIH_MGC 8"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EccRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 252.2; DB 2
Pred. No. 7.3e-42;
0; Mismatches 13
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AA311750 409 bp mRNA linear E EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end,

EST 19-APR-1997

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REFERENCE
AUTHORS
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Best Local Similarity
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B (bases 1 to 409)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fizzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmazos, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fields, C., Fraser, C.M., and Venter, J.C.
                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
AA311750
AA311750.1
                                                                                                                                                                                                                                                             ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7566098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 3018699423
                        ACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCG
                                                                                      TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTNTTCAGATGCCGGCCC
                                                                                                            TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCC
                                                                                                                                                                         GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTGCGGAAGACAGTGG
                                                                                                                                                                                                  GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGG
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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'clone_lib="Jurkat T-cells VI"
'note="Vector: pBluescript SK-; Site_1: EcoRI; Site_
'note="Vector: pBluescript SK-; Site_1: EcoRI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="ATCC (inhost):158964"
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                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                            Score 249.6; DB 1;
Pred. No. 2.3e-41;
0; Mismatches 6;
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BE396606
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM290 row: i column: 19
High muality sequence start: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 2
High quality sequence stop: 656.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 679)
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     GCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGAC 1908
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                                                                                                                                                                                                             ACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGGTTGGCTGTTTCCGGCC-GCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT 1685
                                                                                            TIGCAAAGCATIGGAAICAGACACCACIIGAAGAGGGIGCAGCIGCGGGAGCIGICGGAA 1864
                                                                                                                                                                          ACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAG
                                                                                                                                                                                                                                                                                        AGGGGTTGGCTGTTCCGGCCTGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/lone="IMAGE:3619674"
/tissue_type="Burkitt lymphoma"
/tissue_type="Burkitt lymphoma"
/tissue_type="Burkitt lymphoma"
/tissue_type="Burkitt lymphoma"
/tissue_type="Burkitt lymphoma"
/tissue_type="NIH_MGC_88"
/clone_lib="NIH_MGC_88"
/clone="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into BcoRI/XhoI sites using the following 5'
cloned into BcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/mol_type="mRNA"
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Pred. No. 3.7e-41;
0; Mismatches 7
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REFERENCE
AUTHORS
TITLE
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BE514070
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM330 row: f column: 19

High quality sequence stop: 628.

Location/Qualifiers
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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601316575F1 NIH_MGC_8 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                 CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTT-CTACCGGAAGAGTGTCTGGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                 GCAGAGGTCAGGCAGCATCGGGAAGCCAGGCC 1896
                                                                                                                                                           TTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAA 1864
                                                                                                                                                                                                                                                                                                                                      AGGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT 1686
                                                                                                                                                                                                                                   CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTACTACCGGAAGAGTGTCTGGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Burkitt lymphoma"
/lab host="DH10B (phage-resistant)"
/clome llb="NH1MGC Bit | Note | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 243.2; DB 2; Length Pred. No. 5.4e-40; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                   546
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM330 row: g column: 20
High quality sequence stop: 610.
Location/Qualifiers
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
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BES14188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 610)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                            GAAAAGCATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAAGCTGTCGGAAGC 1866
                                                                                                                                    GGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTT 1806
                                                                                                          GGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTT
                                                                                                                                                                                                                   AGGGGTTGGCTGTTCCCGCCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT
                                                                                                                                                                                                                                                                                                                                                            AGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT
GCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 243; DB 2; 1 larity 100.0%; Pred. No. 5.9e-40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3634987"
/tissue_type="Burkitt lymphoma"
/lab_host="BH108 (phage-resistant)"
/clone_lib="NIH_MGC 8"
/clone_lib="NIH_MGC 8"
/clone_lib="NIH_MGC 8"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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IMAGE:3634987 5',
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Best Local Similarity 76.2%;
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                                                                                                                                                              2885 AGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          262;
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of I
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                           TTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCAC
                                                                                                                                                                                                                                                                            GCCCACGGCCTATTCCCCCTGGTGCGGCCTGCTGCTGGATACCCCGGACCCTGGAGGTGCAG 2884
                                                                                                             TGTGACTACTCAGGTTATGCCCAGACCTCAATTAAGACGAGCCTCACCTTCCAGAGTGTC
                                                                                                                                                                                                                     GCTCACTGCCTGTTTCCCTGGTGTGGGCTTGCTGGACACTCAGACTTTGGAGGTGTTC
                                                                                                                                                                                                                                                                                                                                     GTGGTGAACTTCCCTGTGGAGCCTGGTACCCTGGGTGGTGCAGCTCCATACCAGCTGCCT
     TTCAAAGCTGGGAAGACCATGCGGAACAAGCTCCTGTCGGTCTTGCGGTTGAAGTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="whole brain"
//dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
//dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
//done lib="NHIOB (T1 phage resistant)"
//clone lib="NHI BMAP FYO"
//note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
grimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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/strain="C57BL/6"
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Pred. No. 6.2e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM132 row: i column: 16
High quality sequence stop: 535.
Location/Qualifiers
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National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCA 3108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCTATTTCTAGACTTGCAGGTGAACAGCCTCCAGACAGTCTGCATCANTATATACANG
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                                                                                                                                                                                        AGGGGTTGGCTGTGTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTT 1686
                                           TGCAAAGCA-TTGGAATCAGACAGCACTT--GAAGAGGGTGC-----AGCTGCGGGAGCT 1857
                                                                                                                         GGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCT-GGAGCAAGT 1805
                                                                                                                                                                  GGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGGAGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 779)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:3345111"
/tissue_type="Burkitt lymphoma"
/lab host="DHIDB (phage-resistant)"
/lab host="DHIDB (phage-resistant)"
/clone=lib="NIH_MGC_8"
/clone="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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86.8%;
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                                                                                                                                                                                                                                                                                                                                                       Score 208.6; DB 2
Pred. No. 9.4e-33;
                                                                                                                                                                                                                                                                                                                                        Mismatches
    CTTTGGAAGAGGGTGCTCGCTTGCCGGGAACTTG 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear EST 13-0
clone IMAGE:3345111
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                                                                                                                                                                                                                                                                                                                                                                            Length 779;
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5111 5',
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MEDLINE
PUBMED
                                                                                                                                                           Query Match
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                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hicozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Maramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY775178 mrNA 1
'BY775178 RIKEN full-length enriched, 17.5 da
Mus musculus cDNA clone L930091N09 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res.
22703353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-9216
                                                     GCCGCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 336)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   details.
                                                                                                                                                                                                                                       /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone lib="RIKEN full-length enriched, 17.5 days embryo
whole body"
                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930091N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                  5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     type="mRNA
                                                                                                           0
                                                                                                        Score 203.8; DB 6
Pred. No. 8.3e-32;
0; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokohama, Kanagawa 230-0045,
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d, 17.5 days embryo
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Muridae; Murinae; Mus.
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BY783093
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                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13 (6B), 1273-1289 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12819125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTACCAGGTGTGCGGCC
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                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
                                                     /db_xref="taxon:10090"
/clone="L930172A03"
                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                    location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Tel: 81-45-503-9222
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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BY149368
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                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           whole body"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (house mouse)
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76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
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Pred. No. 3.9e-31;
0; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573
                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                    Matches 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1711 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yang,Isawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
                                                                                                                                              314
                                                                                                                                                                                                                                                                     254 GCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGTGGCCCGAGTGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
GCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTG-CCCAACAC 432
                                                                                                                                              AGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGG 373
                                                                                                                                                                                                                          GCCGACCTTTCCTTCCACCAGGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAG
                                                                       AGACTCTGCGAGCGCAACGAGAAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAG
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 192.2; DB 5
Pred. No. 2.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 326;
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Query Match Best Local Similarity

4.7%; 61.2%;

Score 189.2; DB 5; Pred. No. 1.1e-28;

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REFERENCE
AUTHORS
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ORGANISM
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BU452535
LOCUS
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Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 01612008930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Box 88, Manchester, M60 1QD, UK
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/Clone lib=CCSEQRBN14"
//Clone lib=CCSEQRBN14
//Clone lib=CCSEQRBN15
//Clone lib=CCS
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/lab_host="DH10B"
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                                                                                                                                                                  Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE: (E-mail: seqrefegenoscope.cns.fr - Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
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Tetraodon nigroviridis full-length
CR688161 GI:51186068
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                Conservative
                                                                                     /organism="Tetraodon"
/mol_type="mRNA"
/db_xref="taxon:47144"
/tissue_type="Byes"
                                                                                                                                                                                                                                                                                                                                                                                                                 full-length;
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              Score 186.8; DB 3;
Pred. No. 3.7e-28;
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347 bp mRNA linear EST 25-JAN-200
BR END06B09 Bain Rancourt retinoic acid induced ES cell neural
differentiation subtraction library Mus musculus cDNA clone 06B09
similar to gb|AF073311|AF073311 Mus musculus telomerase catalytic
Department of Biochemistry
University of Calgary
3330 Hospital Drive N.W., C
Tel: 403 220 2888
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                          similar to gb subunit mRNA,
                                                             Contact: Rancourt
                                                                                         21652683
                                                                                                         Funct.
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                                                                                                                                                                  Bain, G., Mansergh, F.C., Wride, M.A., Rancourt, S.L., Ray, W.J., Yoshimura,
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                                                                                                         Integr.
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                                                                                                                                                                                                                                                                                                                            complete
                                                                                                                                      .E. differentiation
                                                                                                           Genomics
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                                                                                                         \vdash
                Calgary,
                                                                                                         (2),
                                              and
                                                                                                                                                                                                                  Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                              Molecular Biology
                                                                                                           127-139
                                                                                                                                          reveals
                                                                                                                                                                                                                                                                                                                            sequence.
                 Alberta, T2N
                                                                                                                                                                      Hance,J.E.,
Y., Tsuzuki,
                                                                                                                                        a substantial
                   4N1,
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[., Gottlieb
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Murinae; Mus
                                                                                                                                        number of
                   Canada
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neural
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequencing by: University Core DNA Services, University of
Laboratories) according to the manufacturer's protocol.
2.5 ug of amplified cDNA from 4./3+ cells was mixed with
50 ug of biotinylated ES cell cDNA, denatured by boiling,
and hybridized for 20 h. Double stranded cDNA containing
biotin were removed by streptavidin/phenol treatment as
described [1]. The remaining subtracted cDNA was mixed
with an additional 25 mg of biotinylated ES cell cDNA,
denatured by boiling, and hybridized for 2 h. The
streptavidin/phenol treatment was repeated and the
remaining cDNA was amplified by PCR [Wang and Brown,
1991]. Two additional rounds of subtraction were repeated
exactly as described above. The cDNA obtained from this
subtraction procedure was digested with EcoR1 and ligated
to pBS II SK+ (Stratagene) followed by transformation
into E. coli DH5 cells. Individual colonies were picked
and the corresponding plasmids were isolated either by an
alkaline lysis miniprep procedure [2], or using the
Qiaprep spin miniprep kit (Qiagen). Sequence analysis was
performed using the Big Dye Cycle Sequencing kit and an
ABI373 sequencer (University Core DNA Services,
University of Calgary). 1. Wang, Z; Brown, DD (1991) A gene
expression screen. Proc. Natl. Acad. Sc i. USA 88,
11505-11509. 2. Sambrook, J; Fritsch, EF; Maniatis T. (1989)
Molecular Cloning: A Laboratory Manual. Cold Spring Harbor
Laboratory Press, Cold Spring Harbor, New York."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNAs corresponding to mRNAs which are upregulated during the neural differentiation of ES cells in vitro, the subtractive hybridization technique of Wang and Brown [1] was employed. Poly(A)+ RNA was prepared from both undifferentiated ES cells and from embryoid bodies which had been cultured for 4 days in the absence of RA followed by an additional 3 days in the presence of 0.5 (M RA (4-/3+ cells). These poly(A)+ RNAs were converted to double-stranded cDNA using the Superscript Choice System (Gibco). Aliquots of both cDNAs were digested with the restriction enzymes Alul and Alul plus RsaI. An adaptor oligo [1] containing an EcoRI site was ligated to the ends of the restricted cDNAs to provide primer binding sites and large amounts of each cDNA population were then produced by the polymerase chain reaction (PCR) as described [1]. Amplified cDNA from undifferentiated ES cells was biotinylated using Photoprobe biotin (Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rancourt@ucalgary.ca; URL:http://www.acs.ucalgary.ca/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARIAD Pharmaceuticals Inc., 26 Landsdowne Street, Cambridge, Massachusetts, 02139-4234, U.S.A.). To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH5 alpha"
/clone_lib="Bain Rancourt retinoic acid induced neural_differentiation subtraction library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EcoR1; Site
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EcoR1; Site_2: EcoR1; Library constructed by Dr. Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/strain="129"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ES) cell"
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ORIGIN

Query Match Best Local Similarity

Score 182.6; DB 2; Pred. No. 2.2e-27;

Length 347;

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KEYWORDS
SOURCE
ORGANISM
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VERSION
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BU377259
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                         source
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BU377259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosc Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST.
Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU377259 880 bp mRNA linear EST 28-NOV-2002 603811228F1 CSEQCHN74 Gallus gallus cDNA clone CheST798g7 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU377259.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. 12 (22),
                                                                                                                                                                                                                                                                                                                                                                                      Simon. Hubbard@umist.ac.uk.
/clone lib="CSEQCHN74"
/note="Organ: kichey + adrenal; Vector: pBluescript II
/note="Organ: kichey + adrenal; Vector: pBluescript II
KS(+), Site 1: EcoRI; Site 2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/mol_type="mRNA"
                                                                                                                                                           /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                          /db_xref="taxon:9031"
/clone="ChEST798g7"
                                                                                                                                                                                                                                                                      strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                          sex="Female"
                                                                                                                                                    host="DH10B"
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RESULT 35
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                                                                                      AUTHORS
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Panopoulou, G., Hennig, S., Groth, D., Krause, A., rouse, A., Hennig, S., Groth, D., Krause, A., rouse, A., Henwig, R., Vingron, M. and Lehrach, H.

New evidence for genome-wide duplications at the origin of the vidence for genome-wide duplications at the origin of the vidence and amohioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                 BI388013 775 bp mRNA linear EST 26-AUG-200: BFL26_002716 Amphioxus 26hr cDNA library (Name convention: BFL26 o: MPMGp531) Branchiostoma floridae cDNA clone MPMGp531A0937 5', mRNA
                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
                                                                                                                                            Branchiostoma.
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                                                                                                                                                                  Eukaryota; Metazoa;
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                                                                                                                 to 775)
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Pred. No. 8.2e-27;
0; Mismatches 203;
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MEDLINE
PUBMED
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3'
Insert Length: 1 Std Error: 0.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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                                                                                                      TGGCTGCGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCT
                                                                                                                                                                                                                            ACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTA
GGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCT 2856
                                                                                                                                                                            CCCACACCTGGACCAGGCTACAGCCTTCCTCTGTACCATGTTGGATGGTATCCCTGAATA
                                                                                                                                                                                                                                                                                  CTGTGGCATGGATGGGTTGCTGCTGCGTCTGGTGGATGACTTTCTGCTGGTGAC 196
                                                                                                                                                                                                                                                                                                                                                                                        TGGGTGCAGCGTTCATCCGGACAAAGTCCTGACCAACTTCCCTGTCCAGCACAGGAATGC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pSport1 (Gibco BRL); Site_1: SalI KpnI, EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OllgodT primed and directionally cloned in pSport1 vector using NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCGCCC (T)15-3' and a SalI 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole embryo"
/dev stage="26 hrs (neurula stage)"
/lab_host="E.coli, Xii blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
/clone_tib="Amphioxus 26hr cDNA library (Name convention:
/potery: Screen (Gibon BBI). Site 1: Sall Kont
/potery: Screen (Gibon BBI).
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/db_xref="taxon:7739"
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
On Dec 18, 2003 this sequence version replaced Contact: Guiguen Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. (bases 1 to 703)

Govoroun, M., Guiguen, Y. and Le Gac, F. Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                    Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Campus de beaulieu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX886589.2
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                                                                                                                                                      /organism="Oncorhynchus mykiss/mol type="mRNA"
/db_xref="taxon:8022"
/clone="tcbk0036c.p.02"
/tissue_type="multi-tissues"
/dev_stage="from embryos to ac/lab_host="DH10B"
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.28.02
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619 bp mRNA linear EST 29-DEC-2003 k0850A03-5 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence. CK392784
                                                                                                                                                                                    1 (bases 1 to 619)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif.
                                    Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                              Contact: Dawood B. Dudekula
                                                                                                                    11544199
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Pred. No. 4.1e-23;
0; Mismatches 266;
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                                                                                                                                                                                                        GGTGTCTGACCTGAGTCTCTCTGGG----TCGGTGTGCTGTAAACACAAGCCCAGCTCCAC
                                                                                                                                                                                                                                                                                                         TCGGTCCCCGAGGTGCCTACTGCA-----
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                                                                                                                                                                                                                                                     GCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC
                                                                                                    ATCTCT----GCTGTCACCACCCCGCCAAAATGCCTTTCAGCTCAGGCCATTTATTGAGAC
                                                                                                                                                   ATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGAC
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CAGACATTTCCTTTACTCCAGGGGAGATGGCCAAGAGCGTCTAAACCCCCTCATTCCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: psPoRT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lqsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 1: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 13 embryos at 8.5-days postcoltum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole embryo including
tissues at 8.5-days postcoitum"
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/db_xref="niaEST:K0850A03-5"
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/lab_host="DH10B"
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GGAAGCCCTGGCCCCGGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCG

Query Match Best Local

Similarity

3.9%;

Score 154.8; Pred. No. 1.0 Mismatches

1.6e-21;

5

Indels

9

Gaps

87

Matches

319;

Conservative

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RESULT 38
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1 (bases 1 to 696)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Ourr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
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Fax: 01612360409
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              /clone_lib="CSEQCHL24"
//clone_lib="CSEQCHL24"
//clone="Organ: brain; Vector: pBluescript II KS(+); Site_1:
//core="Organ: brain; Vector to accommodate cDNA produced with the Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaaag]
[5'aattcttttttttcggatccggggctgcacgc]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simon.Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                     /dev_stage="16 day embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, H
                                                                                                                                                                                                                                                                                                                                              db xref="taxon:9031"
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Rexroad, C.E. 3rd, Lee, Y.; Keele, J.W., Karamycheva, S., Brown, G.
                                                                                                                                                                                                                                                                                                                                                                                                                    CA380121 659344 NCCCWA 1RT Oncorhynchus
                                                                                   Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
                                                                                                                             USDA, ARS, National Center for Cool and Cold Water 11876 Leetown Road, Kearneysville, WV 25430, USA Tel: 304 724 8340 x2129
Fax: 304 725 0351
                                                                                                                                                                                                                               Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J. Sequence analysis of a rainbow trout cDNA library
                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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                                                                                                                                                                                      Contact: Rexroad CE
                                                                                                                                                                                                    Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
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                                                        cross match v0.990329.
Seq primer: AGCGGATAACAATTTCACACAGGA.
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/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
                               1. .668
                                           Location/Qualifiers
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mykiss cDNA clone 1RT49P11_B_H06
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AI824948/c
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 148)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                            AI824948
wb04c01.x1 NCI_CGAP_GC6
                                                                                                                                               EST
                                                                                                                                                                                       mRNA sequence.
  Contact: Robert Strausberg,
                                                                                                                  Homo sapiens
                                                                                                                              Homo sapiens (human)
                                                                                                                                                           AI824948.1 GI:5445619
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Pred. No. 1.3e-20;
0; Mismatches 221;
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  Ph.D.
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GAAGCCAGGCCCGCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGCTG 1945
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/clone="1R749P11 B H06"
/tissue_type="pooled"
/lab host="DH108"
/clone lib="NCCCWA LRT"
/clone lib=NCCCWA LRT"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
   TCCCGCCTCCGCTTCATCCCCAAGACCGAAGGGATG
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AZ972318
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                                               COMMENT
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 423 Std Error: 0.00
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Mio
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 641)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ972318
641 bp DNA linear GSS 27-APR-200
2M0246F07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0246F07 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40UP from Gibco
                                                                    plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                            AZ972318.1 GI:13843545 GSS.
University of Utah
University of Utah
                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                              AZ97231
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/note="Vector: pT773D-Pac (Pharmacia) with a modified /note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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                            Genome
                                                    Weiss
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Best Local Similarity
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                                                                                                                                                                                                                                               1140
                                                                                                                                                                                                                                                                                                                                                                                                                                            1023
                                                                                                                                                                                                                                                                                                                                            1080 вессстреттестветствестетстваннесствесствествественнего политивности
                                                 1260
                                                                                                                                                                                                 396
                                                                                                  456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 ACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCC 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 AACACAAGCCCAGCTCCACATCTCTGCTGTCACCACCCGCCAAAATGCCTTTCAGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0246 row: F column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 641.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rm. 308,
                                                                                                                                                                                                                                                                                              ACCCCTCATTCCTACTCAGCAACCTCCAGCCTAACTTGACTGGGGCCAGGAGACTGGTGG 395
                                                                                                                                        TGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGC 1259
                                                                                                                                                                                                                                                                                                                                                                                                GGCCATTTATTGAGACCAGACATTTCCTTTACTCCAGGGGAGATGGCCAAGAGCGTCTAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGA---CAAGGAGCAGCTGC 1079
                                           AGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAG 1319
                                                                                               TATCGCGTCGATACTGGCAGATGCGGCCCCTGTTCCAACAGCTGCTGGTGAACCATGCAG 515
                                                                                                                                                                                                                                                  AGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCC
AGTGCCAATATGTCAGACTCCTCAGGTCACATTGCAGGTTTCGAACAGCAAACCAACAGG
                                                                                                                                                                                                    AGATCATCTTTCTGGGCTCAAGGCCTAGGACATCAGGACCACTCTGCAGGACACACCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
Chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="UUGC2M0246F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic
/strain="C57BL/6J"
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Pred. No. 9.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 140; Indels
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RESULT 42
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JOURNAL
MEDLINE
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Best Local Similarity
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1 (bases 1 to 875)

2 (bases 1 to 875)

3 (bases 1 to 875)

3 (bases 1 to 875)

4 (bases 1 to 875)

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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU122597 875
603148441F1 CSEQCHL18 Gallus
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BU122597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
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Tel: 01612008930
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                                                                  GGCCTTCGGCTTCGCGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCCCCCGCGGTGCTCGCGCCATCCCCCGGCCCATCTGCTTCCAGCAGTTATCCAGTCA 284
                                                                                                                                                                                                                                                                                                                                                       CGTGCCCTGGGACGCACGGCCGCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCCT
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TGCGTATGGATACTCCTTGCTGGATGAGAACAGTTGTCACTTCAGAGTTTTGCCATCTTC
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/note POTAGE: Small intestine; Vector: pBluescript II
/note Porgan: small intestine; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: Not1; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BsgI and BamHI sites
[5'ggccgcgtgcagcccggatccggatccggaaaaaaag]
[5'aattctttttttcggatccgggctgcacgc]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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strain="Compton Line 15I"
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Pred. No. 4.4e-16;
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gallus cDNA clone ChEST151a12 5', mRNA
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National Institutes of Health, M
Unpublished (1999)
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AGENCOURT 22432746 NIH ZGC 7
5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15246 row: h column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cyprinidomes; Cyprinidae; Danio.
1 (bases 1 to 846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN505902.1 GI:46818526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 756.
                                                                                                                                                                                                                                                                                                                                                                                    quality sequence start:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 588
/clone_lib="NIH_ZGC_7"
/note="Vector: pExpress; Site_1: Not1; Site_2: EcoRV;
/note="Vector: pExpress; Site_1: Not1; Site_2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NHT EGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
                                                                                                                                                                                                   /db xref="taxon:7955"
/clone="IMAGE:7267941"
/tissue_type="whole body"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                  organism="Danio rerio"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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Danio rerio cDNA clone
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Ostariophysi;
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Query Match Best Local S Matches 252

Similarity

57.3%;

0

Score 128; DB 7; Pred. No. 6.5e-16; 0; Mismatches 185

Length 846;

Indels

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RESULT 44
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1 (bases 1 to 813)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Ways,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Bitechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RST17589 Athersys RAGE Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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/organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="ttaxon:9606"
/ceIl line="HTI0800"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression / Inbraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation
                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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RESULT 45
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                                    62
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CA353864
CA353864.1 GI
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoste

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoste

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 632)
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Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J. Semience analysis of a rainbow trout cDNA library and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
Single pass sequencing. Bases called with phred v0.020425.c and
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11876 Leetown Road, Kearneysville, WV 25430, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Rexroad CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene index
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                                                                                                                                                                                                                                                                                                                                                                                                                                cross_match v0.990329
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                                                                                                                                                                                /clone_lib="NUCLWM IN.
/note="Vector: pCMV SPORT6; Site
Library made from pooled tissue f
spleen, muscle, and kidney."
                                                                                                                                                                                                                                                                                 /db_xref="taxon:8022"
/clone="1RT74012_C_H06"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                      organism="Oncorhynchus
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Pred. No. 4.9e-15;
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mykiss cDNA clone 1RT74O12_C_H06 5',
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                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
On Dec 18, 2003 this sequence version replaced
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized
libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 724)
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                                                                                                                                                                                                                                                                                                              Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss (rainbow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX889962.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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                                                                                                                                                                                                                                                                    primer: M13R.
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          /clone_lib="tcbk"
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"
                                                                                                                                 /clone="tcbk0041c.i.20"
/t188ue_type="multi-tissues"
/dev_stage="from embryos to a
/lab_host="DH10B"
                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:8022"
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                                                                                                                                                                                                                        organism="Oncorhynchus mykiss"
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Query Match
Best Local :
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                                                GGATGTGACGGCGCGTACGACACCATCCCCCAGGACAG
                                                                                                                                                    CACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCCTGAGCTGTACTTTGTCAAGGT
                                                                                                                                                                                                          CTCTCCCTCTCTCCTGGGGCTCTACAGTGTGGGGGGTTGACCGACATCCACAGAGTCCTCTC
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GGATGTGAGTGGGGCCTATGACAGTCTACCCACACTCAG
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Unpublished (2003)
On Dec 18, 2003 this sequence
Contact: Guiguen Y Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization
libraries in rainbow trout, Oncorhynchus m BX882610 tcbk Oncorhynchus mykiss cDNA clone tcbk0060c.h.01 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Onco Oncorhynchus mykiss Oncorhynchus mykiss (rainbow trout) BX882610.2 mRNA sequence (bases 1 to 646) GI:42815406 version replaced mykiss of normalized cDNA gi:40127495 Euteleostomi; 20-JUL-2004

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                 RESULT 48
BX315053
                                                                   ACCESSION
VERSION
                                                                                                                   DEFINITION
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 Oncorhynchus mykiss (rainbow Oncorhynchus mykiss Eukaryota; Metazoa; Chordata;
                                                                                                             BX315053 tcay Oncorhynchus
                                                                                 mRNA sequence.
BX315053
                                                                 BX315053.2
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus de beaulieu,
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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/note="Vector: p7773D-pac; AGENAE Rainbow trout
/note="Vector: p7773D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. François PIUMI,
François.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
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/tissue_type="multi-tissues"
/dev_stage="from_embryos_to
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                                                                 GI:42620226
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Pred. No. 3.6e-13;
0; Mismatches 182;
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us mykiss
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Sequence cleaned of vector, adaptator and repetitions. Contact
at sigenasupport@jouy.inra.fr to obtain the chromatogram of thi
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Contact: Guiguen Y
INRA - SCRIBE
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1 (bases 1 to 731)
Govoroun, M., Guiguen, Y. and Le Gac, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCT
CACACCCAAAATGCCTGAAGACTTCAAGGCCATCCAGGCCTAGAGG
                                CAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGG
                                                                                                              TAAGAGGAAGCTGGAGGGAAGCTGGAGGGTTTGAGATTGGCCCGAATCAGACAGGCTGC
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                                                                                                                                                                                                                             GTTGGTTCTGTCCCGTCATCGCCCCCCTCTACTACCATCTCCTCGCTCCGCTACGCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGGAGTACACCAACCATCTAGTCAGACTCTGCAACAAAGGTGTGTCTCTAGGCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: M13R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-pac; Rainbow trout multi-tissues normalized + 1 subtraction (tcay); Clone distribution AGENAR Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Jossas cedex, France, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intes
kidney, liver, muscle, ovary, pituitary, testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="from embryos to adults"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="tcay0029b.n.21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l_type="mRNA"
_xref="taxon:8022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                row: n
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Pred. No. 3.6e-13;
0; Mismatches 182
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KEYWORDS
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BX521269
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Best Local Similarity
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                            3356
                                                                                                                                                                                                                               3236 GCCGCCGGCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGCCACCAAGCATTCCTGCTC
                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further inform sugF, Primer sequence; CTTCTGCTCTAAAAGCTGCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RZPD; IMAGD998M035892.

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;

Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi//esponse?libNo=981 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de
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Contact: Ina Rolfs
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX521269 509 568 bp mRNA linear EST 27-JUN-2003 BX521269 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2373290, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC
                                                                                                                                                                             GCCTCTGGCTCCTTTCCTCCTGAAGCCGCACATTGGCTCTGCTACCAGGCCTTCCTGCTC
                                                                                                                           AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG
                                                                              AAGCTGGCTGCTCATTCTGTCATCTACAAATGTCTCCTGGGACCTCTGAGGACAGCCCAA 262
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UnigeneSet - RZPD2
                                                                                                                                                                                                                                                                                                                                                                                                      performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney, Vector: pME18S-FL3; Site 1: DraIII
(CACCATGTGTG; Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
/clone="IMAGp998M035892 ; IMAGE:2373290"
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lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                     2.8%;
                                                                                                                                                                                                                                                                           Score 113.4; DB 5;
Pred. No. 6.8e-13;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                568;
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REFERENCE
AUTHORS
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AUTHORS
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SOURCE
ORGANISM
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AG363333
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JOURNAL
                                                                                                                                                                                                                                                            Best Local
Matches 6
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AAACTGCTGTGCCGGAAGCTCCCAGAGGCGACAATGACCATCCTTAAAGCTGCAGCTGAC
                                                                                                                                                67
                                                                                                                                                                                                                                                             679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2332)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing : TJ
LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Toyoda,A., Noguchi,H.,
BAC end Sequences of Library MSMg0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus molossinus
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                                 GGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCC 186
                                                                                                             TCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCT 126
                                                                                                                                                                                   CTGCGTCCTGCTGCGCACGTGGGAAAGCCCTGGCCCCCGGGCCACCCCCGCGATGCCGCGCGC 66
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2332
                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : pBACe3.6
: EcoRI
: EcoRI.
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                                                                                                                                                                                                                                                                                                                                                     tissue_type="mixture of kidney and spleen"/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                            clone="MSMg01-165A22.TJ"
sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; (Rodentia;
                                                                                                                                                                                                                                                             0; Mismatches 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library MSMg01
                                                                                                                                                                                                                                                                           Score 112.4; DB 9;
Pred. No. 1.4e-12;
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clone:MSMg01-165A22.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                 Length 2332;
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5 5 5 5 B

266 CCTACGGGGTGCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGCAGCAGCCG 1325	1266
206 AGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCC 1265	1206 1891
46 TCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCC 1205	1146 1831
986 CCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCA 1145	1086 1771
)26 TGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACCAAGGAGCAGCTGCGGCCCT 1085	1026 1711
1025 Heading Control Headi	1 6
06 CTTTGAAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	H 0
46 GACCGAGTGACCGTGGTTTCTGTGTGĞTGTCACCTGCCAGACCCGCCGAAGAAGCCACCT 905	h 6
86 CTGAĠCCGGAGCGGACCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTG 845	0 4
26 GCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCC 785	726 1414
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06 CCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGA 665	0 4
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06 TGCTGCAGAGGCTGTGCGAGCGCGCGAAGAAAGAACGTGCTGGCCGCGCGTGCGCGCGC	
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12666.048 Million cell updates/sec
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AY407351 Mus muscu
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BG917907 602820830
AW276315 XXIDD12.x
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CA353864	BG198331	CN505902	BU122597	AZ972318	AI824948	CA380121	BU139751	CK392784	BX886589	BI388013	BU377259	AW244516	CR688161	BU452535	BY149368	BY784804	BY783093	BY775178	BE268183	CF531258
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ALIGNMENTS

SOURCE ORGANISM RESULT 1 AY407349 LOCUS DEFINITION PUBMED REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS ORIGIN COMMENT FEATURES Query Match Best Local TITLE TITLE JOURNAL JOURNAL source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1826) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. 2 (bases 1 to 1826) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Homo sapiens TERT gene, genomic survey sequence. Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA gene trios Science 302 (5652), 1960-1963 (2003) them based on alignment Homo sapiens (human) AY407349.1 GI:39763320 AY407349 AY407349 Similarity 14671302 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 1. .1826 /gene="TERT" /locus_tag="HCM2861" Location/Qualifiers 39.5%; Score 1584; DB 9; I pred. No. 0; O; Mismatches 242; 1826 bp DNA linear GSS 15-DEC-2003 VIRTUAL TRANSCRIPT, partial sequence, 45 West Gude Drive, Length 1826;

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1629 GGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCC

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279 GARCCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGAACTTGCGGAAACC	S89 GCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTG	2529 ACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGC	2469 TCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAA 841 NMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2409 CGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCC	2349 CCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAC 	2289 CCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGT	601 NUNININININININININININININININININININ	29 TCACGGAGGTCAT	2169 AGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGC	2109 ATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCC	2049 TCAACTACGAGCGGGGCGCGGCGCCCGGGCTCCTGGGGCGCCTCTGTGCTGGGC	1989 TCCGCAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCACTTCACCTCGAGGGTGAAGGCACTGTTCACTCCACCTCGAGGGTGAAGGCACTGTTTCACCTCCACGGGTGAAGGCACTGTTTCACCTCCACGGGTGAAGGCACTGTTTCACCTCCACGGGTGAAGGCACTGTTTCACCTCCACGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCACGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGCGTCTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTTCACCTCCAGGGTGAAGGCACTGTACACTCAACTGAAGGAAG	1929 CCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCG 	hagccaggccgccctgctgacgtccagactccg 	1809 AAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCG	1749 AGACCACGITICAAAAGAACAGGCTCTITITCTACCGGAAGAGTGTCTGGAG	1689 TGCACTGGCTGATGAGTGTGTACGTCGTGGAGCTGCTCAGGTCTTTCTT
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-2003	AY407350 Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence genomic survey sequence.		RESULT 2 AY407350 LOCUS DEFINITION
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	CAGACTTCAAGACCATCCTGGACTGA 3454	3429	Ş
1800	GGAAGCTCCCGGGGACGACGCTGACTGCCCTTGGAGGCCGCAGCCAACCCCGGCACTGCCCT	1741	Db
3428	GGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCAACCCCGGCACTGCCCT	3369	Ş
1740	ACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTC	1681	Db
3368	ACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTC	3309	Ş
1680	TGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGAC	1621	₽
3308	TGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGAC	3249	Ş
1620	CCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCCGGCCCTC	1561	DЪ
3248		3189	Ş
1560	TTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCCTCTGCTACT	1501	В
3188	TTTGGAAGAACCCCACATTTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTC	3129	γQ
1500	TCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAG	1441	망
3128		3069	γQ
1440	TGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCCAACATCTACAAGATCC	1381	망
3068		3009	Ş
1380	AGGCTGGGAAGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCC	1321	뮹
3008		2949	Ş
1320	ACTACTCCAGCTATGCCCGGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGGCTTCA	1261	ДЬ
2948		2889	Ś
1260	ACGGCCTATTCCCCTGGTGCGGCCTGCTGGATACCCCGGACCCTGGAGGTGCAGAGCG	1201	Дb
2888		2829	Ş
1200	. TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCC	1141	р
2828		2769	Ş

REFERENCE AUTHORS

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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AY407350

DNA linear GSS 15-DEC-2003

Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY407350

AY407350.1 GI:39763321

Pan troglodytes (chimpanzee)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1584)

1 (bases 1 to 1584)

1 (Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302 2 (bases 1 to 1584) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

PUBMED REFERENCE AUTHORS

TITLE JOURNAL

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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCC
               CCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCCTCACCTGCAGGAGACCAGCC
                                                                                                                                                           ATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTG
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ilarity 83.1%;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM2861"
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Pred. No. 2e-262;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muri
1 (bases 1 to 1835)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F.,
                                                                                                                   AY407351 1835 bp
Mus musculus TERT gene, VIRTUAL
genomic survey sequence.
AY407351
                                                             Mus musculus
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                                                                                                         AY407351.1 GI:39763322
                                                    Eukaryota;
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                                                                              musculus
                                                     Metazoa; Chordata;
                                                                              (house mouse)
                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                              TRANSCRIPT,
            Thomas, P.,
                                                                                                                                              partial sequence,
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Murphy, B., Kejariwal, A.,

GSS 15-DEC-2003

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1440 3068 1380 3008 1320 1260

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Direct Submission
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This sequence was made by sequencing genomic exons and ordering
them based on alignment
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Inferring nonneutral evolution from human-chimp-mouse orthologous
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Plate: LLAM12208 row: p column:
High quality sequence stop: 646.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 925)
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BM453198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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AGENCOURT 6387556 NIH MGC 71 Homo sapiens CDNA clone IMAGE:5529840
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                                                                                        CTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC
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 TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/note="Organ: uterrus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
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Pred. No. 1.7e-157;
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BU702370.1
EST.
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Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
Unpublished (1999)
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UI-M-FIO-byx-f-12-0-UI.rl NIH_BMAP_FIO Mus
IMAGE:6400523 5', mRNA sequence.
                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                        Seq primer: pYX-5
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/mol type="mRNA"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:6400523"
                                                                                                       ocation/Qualifiers
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Sciurognathi; Muridae; Murinae; Mus
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University of Iowa

Anatomy Project

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Matches 638;
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                             TGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGC 2855
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TTAAGACGAGCCTCACCTTCCAGAGTGTCTTCANAGCTGGGAAGACCATGCGGAACANGC
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/dev_stage="embryo 12.5dpc"
/lab host="PH108 (T1 phage resistant)"
/clome lib="WIH_BMAP_F10"
/site_2: Not I; The library was constructed according SonaTdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA, synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%;
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Pred. No. 1.2e-93;
0; Mismatches 206;
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Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can lound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 416.
                                                                                                                                                                                                                                                                         466;
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Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (Dases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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xv57e03.x1 NCI_CGAP_Lu28
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Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu28"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/ste_2: Notl; Cloned uniddirectionally. Primer: Oligo
Library constructed by Life Technologies."
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/clone="IMAGE:2817244"
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/mol_type="mRNA"
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1 (bases 1 to 492)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
BM824748
                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 492.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                 /note=Torgan: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI; The $225NU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                    /cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                 clone_lib="S22SNU16n1"
                                                                                                                                                                                                                                                                                                                        tissue_type="Ascites"
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Score 445; DB 4;
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0; Mismatches 0;
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18 cDNA clone S22SNU16n1-99-E07
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                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (house mouse)
              /db_xref="taxon:10090"
/clone="!MAGE:4949887"
/sex="female, virgin"
/tissue_type="infiltrating di
/dev_stage="5 months"
/lab_host="BH10B"
                                                                                                                        /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                             Socation/Qualifiers
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 _lib="NCI_CGAP_Mam6"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
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Matches 387; Conser
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA281296
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                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:712562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="germinal center B cell"
/lab_host="DH10B"
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Pred. No. 8.3e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 650 473 8658
Fax: 650 473 7760
Email: pbrandenberger@geron.com
Insert Length: 409 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
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Lebkowski, J and Stanton, L.W.
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1 (bases 1 to 409)
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Mammalia; Eutheria; Primates; Catarrhini; Homınıdae, Homo
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/note="o
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/mol_type="mRNA"
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                                                      GACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCT
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IMAGE:30355988 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/tabsut_type="minute train"
/dev stage="membryo 13 5,14 5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="MIH BMAP FY0"
/clone lib="MIH BMAP FY0"
/step="corpan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; "Vector: pyX- Asc; Site 1: EcoR I;
/note="Torgan: Brain; Mass size fractionated on a 1% agarose
/note gel. First strand cDNA synthesis was primed with oligo-dT
/primer containing a Not I site. Double strand cDNA was
/note gel. First strand cDNA synthesis was primed with oligo-dT
/primer containing a Not I site fraction, ligated
/note size selected according to mRNA size fraction, ligated
/note gelected according to mRNA size fraction, ligated
/note fractionally into pyX-Asc vector. The library tag
/note sequence located between the Not I site and the polyA tail
/note fractional fractions of Membrand Health (NIMH), Hemin Chin, Ph.D.,
/program coordinator."
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/tissue_type="whole brain"
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/strain="C57BL/6"
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73.9%;
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UI-M-FY0-Cgp-C-19-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:30355746 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 649)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NTH BMAP_FYO"
/clone lib="NTH BMAP_FYO"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyx- Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
Site_2: Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:30355746"
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15.

Matches

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REFERENCE
AUTHORS
                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                          RESULT 14
BB618671
                                                                                                                                                                                                                                                                                                                 DEFINITION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 599)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
                                                                                                                                                                                                  EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                           BB618671 RIKEN full-length enriched, 8 c
CDNA clone 5730412M20 5', mRNA sequence.
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BB618671.1
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                                                                                                                                                                                                                                                        GI:16458173
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77.3%;
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61

CACCCTTGCATCTTGGTTCCCGCACGTGGGAGGCCCATCCCGGCCTTGAGCACAATGACC CAGCGCTGCGTCCTGCCGCACGTGGGAAGCCCCTGGCCCCCCGCGACCCCCCGCGATGCCG

120

Matches

403;

Conservative

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Indels

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Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant CDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RJ
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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e mouse tissues
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Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched, 8 days embryo"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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NISC kp11g04.q3 Baker mouse embryo
IMAGE:5409222, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 664) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
cDNA Library Preparation: J. Baker (Stanford University)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramu
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution informat
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XII-Blue"
                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
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GTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAA 1767
                                               TĠĊĀĠĀĠĊĀĊĊĠŦĊŦĠĀĠĠĠĀĠĀĠĠĀŦĊĊŦĠĠĊŦĀĊĠŦŤĊĊŦĠŦŦĊŦĠĠĊŦĠĀŦĠĠĀCĀC
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/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned into salI/NotI sites using the following 5' addaptor: 5'-TCGACCGGTCGG-3'. Size-selected for average insert size 1.8-1.9 kb. Library constructed by J. Baker (Stanford University)."
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This invention describes a novel method for the quantitation of tumour cells in a body fluid which comprises (1) enrichment or isolation of tumour cells in the sample, (2) amplification of mRNA from these cells that encodes the catalytic subunit of telomerase and (3) quantifying the amount of amplified mRNA. The method is applied to tumour cells derived from (micro)metastases, e.g. associated with a wide range of tumours such as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia,

pulmonary carcinoma, cancer of colon or breast etc.

Example; Fig 1A-B; 26pp; German.

y 901 CACCTCTTTGGAGGGTGCGCTCTTGGCACCGCCACTCCCACCCA	GACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC			541 GGCTCCCAGCTACCAGGTAGTGGACCCCGAAGGCGTCTGGGAACGGGC 660 541 TCAGGCCCGGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGAACGGGC 660 601 TCAGGCCCGGCCCCACACGCTAGTGGACCCCGAAGGCGTCTGGGAACGGGC 660 601 TCAGGCCCGGCCCCACACGCTAGTGGACCCCCGAAGGCGTCTGGGAACGGGC 660	81 CCGC 81 CCGC	361 GCTGCTGGÁCGGGGGCCCGCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420 421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGGTGGGGGCTGCTGCG 480	CGAGTGCTGCAGAGGCTGTGCGAACGCGGCGCGAGAACGTGCTGGCCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTGGCGAGGAGGCGCGGAGGAGGAGGAGGCGCGGCGCTTCGGCTGGCGTTCGGCTTGGCGAGGGCGGGGGGGG	ACGCCGCCCCCGCCGCCCCTCCTTCCGCCAGGTGTCCTGCCTG	121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCGCGCGC	GCGCGCTCCCCGCTGCGGCGCCCTGCGGCTGCGGCACCACCACCGCGAGGTGCT 1 GCCGCTGGCCACGCTCCCTGCGGCGCAGGCGCGCGCGCGC	0 0 0	Sequence 4015 BP; 665 A; 1363 C; 1273 G; 714 1; 0 0; 0 00001; Query Match 100.0%; Score 4015; DB 2; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	equence encodes a human telomerase protein catalytic d
Db 1981 CAGAACGTTCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040 2041 CAGCGTGCTCAACTACGAGCGGGGCGCGCGCCCCGGCCCTCGTGGCGCGCCTCGGGCGCCCCGGCCTCTGGGCGCGCGCGCGCGCTCTGGGGCGCGCGCGCTCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTGGGGGG	Qy 1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGGGGGC 1980	GAAGTIGCAAAGCA I IGGAAI CAGACAGCAC I GAAGAGCCCGCCCTGCTGACGTCCGACTCCG	1/41 TGTCACGAAGCCACCTILCAAAACAACAACAACAACAACAACAACAACAACAACAAC	1621 G		1501 C 1501 C	Db 1381 CACAGACCCCCGTCGCCTGGCAGCCTCCCCCAGGCCTCCAGGCA 1440 140 CACAGACCCCCGTCGCCTGGCAGCAGCAAGCAAGCAAGCA	Oy 1321 AGCCGGFGCTCGGCGGAGAAAGCCCCCAGGGCTCTGTGGCGGAGGAGGAGGA 1380 Db 1321 AGCCGGTGGTCCGCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA 1380 Oy 1381 CACAGACCCCGTCGCCTGGTGGAGGTGCTCCGCCAGGACAAGCACCTGGCAGGTGTA 1440	1261 G 1261 G	Oy 1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260		1021	Db 961 GCACCACGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020

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Human telomerase reverse transcriptase (hTRT) cDNA

Telomerase reverse cancer; ss. transcriptase; human; hTRT; cell proliferation;

Homo sapiens

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Matches 4015;
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The present sequence encodes a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention. The specification describes a method for activating a Tlymphocyte, comprising contacting the Tlymphocyte with a dendritic cell that expresses a TRT peptide in the context of a MHC class I or MHC class I molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TRT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune respons
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1991 CAGAAGGTTCCGCAGAGAAAAGAGGGCCGAGCGTCCACCTGCAGGGGTGAAGGCACTGTT 2040 2041 CAGCGTGTCAACAAACACGAGGCCAGCGCCGGCGCCGGCGCCCGGGGCCCCTGTGTCCTGGGCCCCCC

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RESULT 4
AAH45901
ID AAH4
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AC AAH4
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AC Huma
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DT 06-S
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DE Huma
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Huma
 Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
                       Human hTERT gene.
                                                                 AAH45901;
                                                                                    AAH45901 standard;
                                            06-SEP-2001
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2524. .2637
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2615. .2631
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1825. .2005

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2638. .2709
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number= 12
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note=""AAH45906"
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note= "primer SYC1118 (AAH45905) binding site"
3342. .2437
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the hTERT gene encoding the catalytic subunit of the human telomerase, comprising 16 exons, which is useful in a method for quantitating hTERT mRNA. The method is useful for detecting the presence of beta-region (a 182 nucleotide region consisting of exons 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis of cancer. The method provides an accurate measure of telomerase activity by selectively measuring mRNA that encodes an active hTERT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quantitating expression of mRNA encoding hTERT, the catalytic subunit of telomerase, as an indicator of cancer, by amplifying RNA using primers complementary to hTERT gene sequence and quantitating amplified products
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CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCTGCTCTTTGTGCTGGT
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                                                        GCTGCTGGACGGGGGCCCGGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA
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CTGCTGCTGCTGGATACCCGG CTGCTTGGATTACCCGG CTGCTTGGATTACCCGG CTGCTTCTGGAGTACCCGG CTGCTTTTGGAGTCTCTG AAACTCTTTTGGAGTCTTG AAACTCTTTTGGAGTCTTG AAACTCTTTTGGAGTCTTGAC CTGCCCATGTATTGTGCTTTGAC CTGCCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGCCTTCCACTCCCC 3721 GGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCC 3721 GGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCC 3781 CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTG	3661 GAGTO 3661 GAGTO	3601 3601	3541 CACA 3541 CACA	3481 3481	3421 3421	3361 G 3361 G	3301 3301	3241 CGC 3241 CGC	3181 CTGC 3181 CTGC	3121 3121	3061 3061	3001	2941 CGG 2941 CGG	2881 GCA 2881 GCA	2821 2821	Qy 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	Qy 2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA

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                                                                                                                                                  The invention relates to animal tissues with carbohydrate antigens that are compatible for transplantation into human patients. The mammalian cell is inactivated homozygously for expression of alpha(,3)galactosyltransferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue with carbohydrate antigens that are compatible for transplantation into human patients. The present sequence is human telomerase reverse transcriptase (TERT) cDNA used in the invention
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P-PSDB; AAE29226.
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                                                                                                                Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
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Discrimination of a cancer cell in a sample tissue, comprises determining the expression level of a reverse transcriptase component of telomerase using a hybridization assay.
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Claim 2; Page 9-10; 16pp; Japanese

The present invention relates to a method for the discrimination of a cancer cell in a sample tissue, which involves determining the expression level of a reverse transcriptase component of telomerase in a cell constituting the sample tissue by an in situ hybridization of the mRNA of the enzyme, and judging a cell showing a higher expression level than that of the reverse transcriptase component of telomerase in a normal cell to be a cancer cell. The present sequence is a human DNA used in the exemplification of the invention

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Length 4015;

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Novel nucleic acid encoding or comprising interfering RNAs which target telomerase RNA, useful for inhibiting telomerase activity for treating cancer, infertility and disorders of the immune system.

Disclosure; Fig 3; 52pp; English.

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The present sequence is that of human telomerase reverse transcriptase (TERT) cDNA. The invention relates to the discovery that double-stranded interfering RNAs, such as short interfering RNAs (SiRNA), which target telomerase RNA or TERT mRNA are capable of inhibiting telomerase activity. Inhibition of telomerase in cancer cells leads to telomerase shortening, end-to-end chromosomal fusion, and apoptosis. Interference of telomerase activity can also be used for treatment of infertility, for contraception or sterilisation, for immunosuppression, for treatment of yeast, parasite and fungal infections, and in antiinflammatory therapies. As telomerase is active in a limited number of cell types, e.g. tumour cells, germline cells, certain stem cells of the haematopoietic system. T and B cells, sun-damaged skin, and proliferative cervix, most normal cells are not affected by telomerase RNA interference therapy

Sequence 4015 B₽; 663 A; 1363 C; 1275 G; 714 T; 0 u; o Other;

Query Match Best Local S Matches 4015

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                                                                     Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome vulnerary; antiulcer; epithelial cell migration promoter; wound; epitheliastion; surgical incision; ulcer; epitheliastion; kkin wound; lesion; burgical incision; ulcer; epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other apidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence encodes human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a vector encoding telomerase reverse transcriptase (TERT) an excipient or device, or comprises telomerised epithelial cells on microparticle or a matrix suitable for topical administration or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for treating wounds and enhancing epithelization of a skin surface, comprises vector encoding telomerase reverse transcriptase or telomerized epithelial cells on a microparticle or a matrix.
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01 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1	Ş
41 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCC	DЬ
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2001 GCAGNGCOMINCICCAGCIA GCCCCCCATCIAC CANAGCCCAGTCICCACCII CANCAGCAGAGCCAGTCICCACCII CANCAGCAGAGCCAGTCICACCII CANCAGAGCGACTACIACAGAGCCAGCTCCACCCATCAACCC 2940 2881 GCAGAGCGACTACTCCAGGAACATCCCGGACCTCCATCAAGAGCCAGTCTCACCCTTCAACCC 2940	5 B &	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860 	용 <i>성</i>
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The invention relates to the generation of primary preadipocyte cell strains that expresse telomerase reverse transcriptase (TEXT the catalytic subunit of telomerase), and maintain and/or enhance replicative potential and maintain adipogenic capacity of the cell. This sequence represents the gene encoding the TERT protein. The cell strain can be used in research to study all aspect of adipogenesis, especially in relation to researching treatments for e.g. obesity. The cell can also be used to identify adipogenesis modulators for use as therapeutic agents
                                                                                                                    New primary preadipocyte strain expressing telomerase reverse transcriptase, useful in research applications, screening assays, clinical applications, and in the administration of therapeutic a particularly for obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gene; ds; human; telomerase reverse transcriptase; primary preadipocyte cell; adipogenesis; obesity; anorectic; adiponectin; insulin.
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2941 CGCCTCAAGGCTGGGAACATCCTTGCGCAACATCTTTGCGGTTCTGCGCTTCAAGTGTTTGCGGTTCTTGCGGTTCTTGCGGTTCTTGCGGTTCTTGCGGTTCTTGCGGTTCTTGCGGTTTTGCAACTCTTTTGGGGTTCTTGCGGTTGCAACTTCTTTGGGGTTCTTGCGGTTGCAACTTCTAAGTTG 3001 TCACAGCCTGTTTCTGGATTTGCAGGTTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	B & B & B &	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCGCCTGACGTCCAGACTCCG 1920
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2821 GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGGATACCCCGGACCCTGGAGGT	당 상	681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTGCAGGTCTTTCTT
2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	QY Db	681 CAAGTTCCTGCACTGGCTGAGTGCGTGTAACGTCGAGGTGCTGCGTGAGGAGATCCTGTTTA 174
2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA	Db Qy	501 GLICITUSCISCASSAGCISACSIGSAAGAIGANGCAIGCGGGAGAGAGCISCGGAGAGAGCACCGTCTGCGTGAGGAGATCCTGGC 16
2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCTCACCCACGCGAAAA	Db Qq	561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG 1
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2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG	QQ VQ	381 CACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA 14
2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	Qy Db	321 AGCCGGTGTCTGTGCCCGGGAGAAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGAAGAAGA 138 321 AGCCGGTGTCTGTGCCCGGGAGAAAACCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGAAGAA 138 321 AGCCGGTGTCTTTGCCCGGGAAGAAGCCCCCAGGGCTCTGTGGCGGCCCCGAGGAGAAGA
2341 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGA	D Q	261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC 1
81	D Q	GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC
21	D 45	1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT 1200
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	D~ 8	961 GCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020
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             reverse transcriptase; TERT; enzyme; RNA interference;
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antiinflammatory; human; gene therapy; gene; ss.
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20-FEB-2002; 2002US-0359196P.
22-MAY-2002; 2002US-0383195P.
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Novel double-stranded short interfering RNA having sense and antisense nucleic acids which are complementary to each other and to target nucle acid e.g., telomerase RNA or mRNA encoding telomerase reverse transcriptase. target nucleic

Disclosure; Fig 3A-B; 37pp; English.

The present sequence is that of human telomerase reverse transcriptase (TERT) cDNA. The invention relates to the discovery that double-stranded interfering RNAs, such as short interfering RNAs (siRNA), which target telomerase RNA or TERT mRNA are capable of inhibiting telomerase activity. Inhibition of telomerase in cancer cells leads to telomerae shortening, end-to-end chromosomal fusion, and apoptosis. Interference of telomerase activity can also be used for treatment of infertility, for contraception or sterilisation, for immunosuppression, for treatment of yeast, parasite and fungal infections, and in antiinflammatory therapies. As telomerase is active in a limited number of cell types, e.g. tumour cells, germline cells, certain stem cells of the haematopoietic system, T and B cells, sun-damaged skin, and proliferative cervix, most normal cells are not affected by telomerase RNA interference therapy

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

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ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA
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(HUAN/) HUANG C:
(LINM/) LIN M C M.
(KUNG/) KUNG H.
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                                           WPI; 2004-089418/09.
P-PSDB; ADG85224.
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4015; Conservative (
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CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as given in specification, other than human telomerase reverse transcriptase CC (hTBRT) or octamer binding transcription factor (Oct)3/4, or a marker CC (MR2) such as cripto or podocalyxin-like protein and hTBRT and/or Oct3/4 (CC or second marker chosen from (MR2). Also included are maintaining (M2) pPS cells in a pluripotent state (involves causing them to express one of the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical (CC pare zinc finger protein SZF1-1 or zinc finger protein of cerebellum (CC ZIC2, or any other marker (MR4) chosen from PHD protein Jade-1), CRAB-Zinc finger protein (ZNF300), etc., as given in the specification), causing them to express one of the markers chosen from CC (MR3) or (MR4) (or markers chosen from EATA binding protein in the specification), maintaining pPS cells to differentiate into a particular (CC promoter element binding protein (COPBB), etc., as given in the collection that is encoded by a gene that down-regulated upon CC (MR3) or (MR4) (or markers chosen from GATA binding protein in the specification), causing pPS cells in a pluripotent state (involves culturing pPS cells or their progeny in the presence of a normally CC secreted protein that is encoded by a gene that down-regulated upon CC (inferentiation of human embryonic stem (hBS) cells, chosen from CC (inferentiation of hES cells, chosen from PSI protein gene, Tax (CC gene, etc., as given in the presence of a normally CC gene, etc., as given in the specification), causing sequence to be preferentially expressed in undifferentiated pps cells, causing an encoding sequence to be preferentially expressed in undifferentiated pps cells, causing an encoding sequence consoling (MS) differentiated cells from less differentiated cells from any consoling cells expressing a surface marker chosen from any cone of MR1 from cells not expressing the marker), causing pPS cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assessing culture of undifferentiated primate pluripotent stem cells by detecting expression of markers e.g., Zic family member 3, other than human telomerase reverse transcriptase/octamer binding transcription
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(GOLD/)
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                                                                                                                                    TCAGGCCCGGCCCCCCCCCACACGCTAGTGGACCCCCGAAGGCGTCTGGGATGCGAACGGGC
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Qy 2941 CGGCTTCAAGGCTGGGAAGAACATGCGTCGAAACTCTTTGGGGTCTTGCGGCTGAAGTG	a—a	2821 G 2821 G	2761 G 	701	2641 G 2641 G	2581 C	2521 C 2521 C	2461 C 2461 C	2401 G 2401 G	2341 2341	2281	2221	2161	2101	2041	981	1921 1921 1981

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The encoded protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense modeleic acids inhibit telomerase action (by binding to specific mRNA), mucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase
                                                                                                                                                    Query Match
Best Local Similarity
Matches 4015; Conserv
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26-MAR-1998;
14-APR-1998;
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RESULT 14
ABL53711
ID ABL53
XX ABL53
XX ABL53
XX HIMMAN
XX HTERT
XW VACCI
XX VO200
PN WO200
XX VO200
PN T7-AU
XX 17-AU
XX 17-AU
PR 17-AU
P Human telomerase catalytic subunit hTERT cDNA ABL53711 standard; cDNA; 4070 17-JUN-2002 (first entry) BP.

hTERT; telomerase; reverse transcriptase; immortalisation; human; vaccine; enzyme; gene; ss.

28-FEB-2002 WO200216555-A2

17-AUG-2001; 2001WO-GB003726.

17-AUG-2000; 17-AUG-2000; 2000GB-00020246. 2000US-0225734P.

(UYWA-) UNIV WALES COLLEGE OF MEDICINE.

ន Kipling DG, Wilkinson G, Mcsharry B, Skinner Į

WPI; 2002-315462/35

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Novel hTERT-immortalized cell line (human telomerase reverse transcriptase) useful for human vaccine production and prepa antigen, such as a virus or virus-derived agent. preparation Ģ,

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The present sequence is that of hTERT cDNA in plasmid pGRN121. hTERT is C the catalytic subunit of human telomerase. Claimed immortalised cell lines for use in vaccine production are adapted to express hTERT.

C liles for use in vaccine production are adapted to express hTERT.

C Sultable cell lines comprise human diploid fibroblasts, e.g. MRC-5 or W138 cells, transfected with hTERT cDNA or infected by a retrovirus carrying hTERT cDNA, and are capable of supporting antigen production. A method for preparing such cell lines using recombinant techniques is provided. The cell lines are also used as a diagnostic test for the presence of a virus, such as human cytomegalovirus, and to determine the efficacy of antiviral agents by testing the capability of a modified virus containing a reporter gene to infect the cells. The cell lines have the ability, which can be impaired in cell lines immortalised by other methods, of being able to support viral replication. The cells remain comphologically suitable for viral/vaccine cultivation
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Best Local Similarity
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	3960	3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG	•
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	3780	3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCCACATAGGAATAGTCCATCC	Ŭ
•	3780	3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCCATAGGAATAGTCCATCC	•
	3720	3661 GAGTGTCCAGCACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCCGCCTCCACCCCA	Ū
	3720	3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA	•
	3660	3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT	•
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	3600	3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGATTGGCCGAGGCCTG	·
	3600	3541 CACACCCAGGCCCGCACGCTGGGAGTCTGAGGCCTGAGTGAG	•
	3540	3481 GAGCAGACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG	-
	3540	3481 GAGCAGACCAGCAGCCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG	•
	3480	3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA	-

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Search completed: October 30, 2004, 00:00:24 Job time: 1776 secs

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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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GCGCGCTCCCCGCTGCCGAGCCGTGCGCTGCCTGCGCAGCCACTACCGCGAGGTGCT 120	CCCCGGCCACCCCGCGATGCC 60	; Length 4015; ; Indels 0; Gaps 0;	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 134, Appli Sequence 173, Appli Sequence 174, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 100, Appli Sequence 5, Appli Sequence 3, Appli

1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT 1200	1081 GCCCTCCTTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080	961 GCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGACGAAGAAGC 900	781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGGCAGTGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG 720	601 TCAGGCCCGGCCACACACGCTAGTGGACCCCGAAAGGCGTCTGGGATGCGAACGGGC 660	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC 600	481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT 540	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGGCGGGGGGGTGGGGGGTTGCTGCCG 480	361 GCTGCTGGACGGGGGCCCGCGGGGGGCCCCCCGAGGCCTTCACCACCACCACCAGCGTGCGCAGCTA 420	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360	241 ACGGCCGCCCCCGCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCCTG	181 GGACCCGGCGCTTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGC	121 GCCGCTGGCCACGTTCGTGCGGCGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180
221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2221 GENNAGETTANGETTINICANGGENGATONAGGEGGGGGGGGANGACCATCCCCCA 2161 GCCGCCTGAGCTGTACCTTGTCAAGGTGATGTGACGGGGGGGG	2101	2041 CAGUSTICAACTACUAGUGGUGGUGGUGCUCUCTGGGUGCTCUTTGGGUGCTCTUTTGGGUGCTCTUTTGGGUGCTCTUTTGGGUGCTCTUTTGGGUGCTCTTGTGGTGGGGGUGCGCCTCCTTGGGGGGCCTCTTGTGGTGGGGGGGG	1991 CAGANCG I CCGCAGAGANANAGGCCCGGGGGGGGGGGGGGGGGGGGG	1921 CITCATCCCCAAGCCTGACGGGCCGACTGGGACACTGGACACGGCTGCAAGCCTGGGAGGCTGCGGCCGACGCGGCCGACGCGCGCCGACGCGCGCCGACGCGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCCGACGCGCACGCGCCGACGCACGCGCACGCGACGCGCACGCACGCGACGCGCACGAC	1861 GERRAT CAGGEAGACHAGCAGGAGCAGGCCCCCCCCCCCCCAGACCCCGACCCCCC	1801 CAAGTTGCAAAGCATTGGAATCAGACAGCAGGGGGGGGGG	1741	1681 CAAGIICCIGCACIGGIGGAGIGGIGGAGCIGCICAGGICIIICII	1621 GAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGCTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGCTGAGGAGATCCTGGCCGCAGAGCACCGTCTGCGCGCAGAGCACCGTCTGCGCGCAGAGAGATCCTGGCCGCAGAGCACCGTCTGCGCAGAGAGATCCTGGCCGCAGAGCACCGTCTGCGCAGAGAGATCCTGGCCGCAGAGCACCGTCTGCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCGCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAGAATCCTGGCCAGAGAAATCCTGGCCAGAGAAGAAATCCTGGCCAGAGAAGAAATCCTGGCCAGAGAAGAAATCCTGGCCAGAGAAGAAATCCTGGCCAGAGAAGAAAAAAAA	1561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTGGCCGGGAGTGAGCGCGAGGAGAGAGA	1501 CARCGARGECEGETICETENGGARGENECANGGITEATETETETETETETETETETETETETETETETETETE	1441 CGCCTTCGTGCGGCCTGCCTGCGCTGGTGCCCCCAGGCCTCTGGGGCTCCAAGCA 1441 CGCCTTCGTGCGGGCCTGCCTGCGCCTGGTGCCCCCAGGCCTCTGGGGCTCCAAGCA	1381 CACAGACCCCCGTCGCCGGCGAGCCGAGCCAAGCCGTGCCCGAGCAGACCAGAGCCCCTGGCAGGTGTA		1261 GTGCCCTACGGGGTGCTCCAAGACGCCTCTGGTGGAGCCCGGGTCACCCCAGC	1201

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APPLICANT: Morin, Gregg B.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Sul
FILE REFERENCE: 018/258c
CURRENT APPLICATION NUMBER: US/09/990,080
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 09/052,864
PRIOR APPLICATION NUMBER: US 09/052,864
PRIOR TILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
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                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human
JS-09-990-080-1
Query Match 100.0%; Score 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches
                                                                                                                         LENGTH: 4015
TYPE: DNA
ORGANISM: Homo
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NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hTRT"

/note= "human telomerase reverse

transcriptase (hTRT) catalytic protein
component"

SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224
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Best Local Similarity 100.0%;
Matches 4015; Conservative 0
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APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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TOPOLOGY: linear
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US-09-953-052-1
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Patent No. US20020173476A1
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFFICATION: «Unknown»
PRIOR APPLICATION DATA:
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                           APPLICATION NUMBER: US 08/912,951
RILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
RILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                             FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/052,919 FILING DATE: <Unknown>
                                                                                                                             APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                                                                                            APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
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Nakamura, Toru
Chapman, Karen B.
 DATE:
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NUMBER: US 08/974,584
19-NOV-1997
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NAME/KEY: CDS

I.OCATION: 56..3454

OTHER INFORMATION: /pi

transcriptase (hTRT)"

SEQUENCE DESCRIPTION: SEQ ID

US-09-953-052-1
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Best Local Similarity
Matches 4015; Conserv
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELEPHONE: (415) 576-0200
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RESULT 5
US-10-053-758-224
; Sequence 224, Applicati
; Publication No. US20030
; Publication No. US20030
; GENERAL INFORMATION:
                        I LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
sequence DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
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INFORMATION FOR SEQ ID NO: 224
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                FALCA REFLICATION NUMBER: US/08/854,050
PILLING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILLING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILLING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILLING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILLING DATE: 10-CGT-1997
APPLICATION NUMBER: US 08/724,643
FILLING DATE: 01-CGT-1997
APPLICATION NUMBER: US 08/724,643
FILLING DATE: 01-CGT-1996
AFTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend
STREET: Two Embarcadero Center, 8
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                                                                                                                                                                                                          MOLECULE TYPE: cDNA FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
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OF INVENTION: NO. US20030032075Alel Telomerase
R. OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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5. US20030032075A1
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Lingner, Joachim
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  Length 4015;
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1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080	961 GCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGC 900	781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCACCCGGGCAGGAC 840	721 GAGGCGCGGGGCAGTGCCAAGCCGAAGTCTGCCCGAAGAGGCCCAAGAGGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCCAGCCCCGGGTGCGAG 720	601 TCAGGCCCGGCCACCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660	541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC 600	481 CCGCGTGGGCGACGTGCTGGTTCACCTGCTGCACGCTGCTGCGCGCTCTTTGTGCTGGT 540	421 CCTGCCCAACACGGTGACCGCACTGCGGGGGGGAGCCGGGGGGGG	361 GCTGCTGGACGGGGCCCGCGGGGGGCCCCCCCGAGGCCTTCACCAGCCAG	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360	241 ACGGCCGCCCCCCCCCCCCCCCCCCCCCCCCAGGTGTCCCTGAAGGAGCTGGTGGC 300	181 GGACCCGGCGCCTTTCCGCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCCCTGGGACGC 240	121 GCGCTGGCCACGTTCGTGCGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180	61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120	1 GCAGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCACCCCCGCGATGCC 60 1 GCAGCGCTGCGCTGCGCACGTGGGAAGCCCTGGCCACCCCCGCGATGCC 60	Gaps
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2101 CCTGGACGATATCCACAGGGCCTGGGGGGCACCTTCGTGCTGCGTGCG	CAGCUSTOCINACIACUAGOCOGOCOGOCOCOCCOCCOCOCOCOCOCOCOCOCOCOC	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	1921 CTTCATCCCCAAGCCTGACGGGCGACGACTGGACCACTGGACTACGTCGGGGAGC 1980 1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980 1921 CTTCATCCCCAAGCCTGACGGGCTGCTGCGACCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980	GAAAGCNGAAGGTCAAGCAATCGGGAAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	CAAGITIGCAAAGCAITIGGAATICAGACAGCACTIGAACAGGGTGCCAGCTICCGGGAGCTGTC 1	GICACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG	CAAGITICTIGCACTIGGTIGAIGAGIIGTIGGTICGAGCIIGCTICAGGIICTITICTTITA		GALTELUCE LIGENSWASE LIGHEN GARACH INNO GENERAL TOCKSTOLING EL LIGHEN LIGHEN GARACH INNO GENERAL TOCKSTOLING EL LIGHEN GARACH INNO GENERAL TOCKSTOLING EL LIGHEN LIGHEN GARACH INNO GENERAL TOCKSTOLING EL LIGHEN GARACH EL LIGHEN GARA	CARCGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCTTGGGGAAGCATGCCAA 15		CONCERNO CONCERNO CONTROL CONT					1081 GCCCTCCTTCCTAGCTCAGGCCCTGAGGCCCAGCCTGACTGGCGCAGGTTGGCAGGCTCGTGGA 1140	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080

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                                                     CCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG
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                                                                                               AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG
                                                                                                                           CAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTTGCCTTCCACCCCCACCACCATCC
                                                                                                                                                                                                                   GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA
                                          CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG
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US-10-208-243-1

| US-10-208-243-1
| Sequence 1, Application US/10208243
| Publication No. US20030044394A1
| GENERAL INFORMATION:
| APPLICANT: Gaeta, Federico C.A.
| APPLICANT: Geron Corporation
| TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
| TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
| TITLE OF INVENTION: Response to a Telomerase Antigen
| FILE REFERENCE: 015389-003500PC
| CURRENT FAPLICATION NUMBER: US/10/208,243
| CURRENT FILING DATE: 2002-07-30
| PRIOR APPLICATION NUMBER: US/09/675,321
| PRIOR APPLICATION NUMBER: US 60/112,006
| PRIOR APPLICATION NUMBER: US 60/112,006
| PRIOR APPLICATION NUMBER: US 60/112,006
| PRIOR APPLICATION NUMBER: WS 60/112,006
| PRIOR FILING DATE: 1998-03-30
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: Patentin Ver. 2.0
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Qy 721 GAGGCGCGGGGCAAGTGCCAAGATCTGCCCAAGAGGCCCAAGAGCCCAAGAGCCAAGAGCCCAAGAGCCTAGCCC 780	Qy 601 TCAGGCCCGCCCCCCACACGCTAGTGGAAGGCCTTGGGATGCGAACGGGC 660	481 CCGCGTCGGCGACGACGACGACGACGACGACGACGACGACGACGAC	361 GCTGCTGGACGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCCGTGCTGCGGGGGCTGCTGCTGCG [Qy 301 CCGAGTGCTGCAGAGGCTGTGCGAGGCGGGGGGGGGAAGAACGTGCTGGCCTTCGGCTTCGC 360	Db 181 daAccccaccacccccccccccccaccacccacccaccacc	Qy 121 GCGGTGGGCACGTTCGTGCGGGGCGCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180	61 GCGCGCTCCCCGAGCCGTGCGCTGCCTGCGCAGCCACTACCGCGAGGTGCT 1	Query Match 100.0%; Score 4015; DB 14; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GCAGCGCTGCGTGCGCACGTGGGAAGGCCTGGGCCACCCCGGGATGCC 60	; NAME/KEY: CDS ; LOCATION: (56)(3454) ; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) US-10-208-243-1	; SEQ ID NO 1 ; LENGTH: 4015 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: Homo sapiens
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		TCTG 258	521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTC	
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		246 246	401 GACCAGCC	2 24
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RESULT 7
US-10-054-295-224
; Sequence 224, Application US/10054295
; Publication No. US20030044953A1
; PUBLICANTION:
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
; Chapman, Karen B.

Query Match Best Local Similarity 100.0%; Score 4015; DB 14; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GCAGCCTCCCGCTCCTGCTGCTGCGCAAGCCCTGGCCCCGGCAATGCC 60 Db 1 GCAGCCTCCCCGCTGCTGCTGCTGCAAGCCCTGGCCCCGGCAACCCCCGCGATGCC 60 Qy 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTGCTGCGCAAGCCACTACCGCGAAGTGCT 120 Db 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTGCTGCGCAGCCACTACCGCGAAGGTGCT 120 Qy 121 GCCGCTGGCCACGTTCGTGCGGCGCTCCCTGCTGCGCAGCTGCTGCAGCGCGG 180 Db 121 GCGCTGGCCACGTTCGTGGGGCGCCTGGGGGCCCAGGGCTGGTGCAGCGCGG 180 Qy 181 GGACCCGGCGCTTTCCGCGCGCTGGCGGCCCAGTGCCTGGCGGCTGGTGCAGCGCGG 180 Db 161 GGACCCGGCGCTTTCCGCGCGCTTGGTGGCCCTGGGGGCTTGGTGCAGCGCG 240 Natches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; Indels 0; Gaps 0; Natches 4015; Conservative 0; Mismatches 0; Indels 0; In	FEATURE: CLUMP (FEATURE: CDS) (NAME/KEY: CDS) (LOCATION: 563454 (OTHER INFORMATION: /product= "hTRT" (/note= "human telomerase reverse (transcriptase (hTRT) catalytic protein (component comp	REGISTRATION NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 015389-002930US TELEPROMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 224: SEQUENCE CHARACTERISTICS: LENGTH: 4015 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA	FILING DATE: 18-Jan-2002 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/854,050 FILING DATE: 4Unknown APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/ACENT INFORMATION: NAME: Apple, Randolph T.	Morin, Gregg B. Harley, Calvin Andrews, William H. TITLE OF INVENTION: NO. US20030044953Alel Telomerase NUMBER OF SEQUENCES: 225 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 9411 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/10/054,295
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RESULT 8
US-10-054-611-224
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Nakamura, Toru
Chapman, Karen B.
Morih, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALECHLIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech
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Best Local Similarity
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NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
                                     TCAGGCCCGGCCCCCCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660
                                                                                                   GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC
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Pred. No. 0;
0; Mismatches
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2821 GCCGGCCTACTTCCCCTGGAAGACCTCCTGCTGGATACCCCGGACCCCTTGGAGGT	1681 CAAGTICCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTCTT	•
, p, p	1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	- 1
, p	1561 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTGTGGCTGCGCAG 1620	· ·
, p	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560	· `
	1500	· `
р р	1381 CACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA 1440	•
	1321 AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA 1380	•
341	1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACCCCAGC 1320	
	1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260	
	1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCCGCAGGTTGCCCGCCT 1200	
	1081 GCCCTCCTTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	
	1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080	
0-0	961 GCACCACGGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020	
, 12	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCACTCCCACCCA	
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Sequence 1, Application US/10105963

Publication No. US20030068818A1

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Schiff, J. John
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Animal Tissue with Carbohydrate Determinant Selection System 1
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT APPLICATION NUMBER: US 60/277,811
PRIOR APPLICATION NUMBER: US 60/277,811
PRIOR APPLICATION NUMBER: US 60/277,811
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(34
; OTHER INFORMATION:
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TYPE: DNA
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	rctccctggggaagcatgccaa 1560	1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA	유 상
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	ACAGCAGCCCCTGGCAGGTGTA 1440	1381 CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGI	β & δ
	rggcggcccccgaggaggagga 1380	1321 AGCCGGTGTCTGTGGCCGGGAGAAAGCCCCAGGGCTCTGTGGCGG	B 8
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	GCTGCTTGGGAACCACGCGCA 1260	1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA	g V
2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGCTTACTGCGTGCG	TCCCCGCAGGTTGCCCCGCCT 1200	1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTG	D Q
2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCATCATCAAACCCCAGAAAAAACACGTACTGCGTGCG	TGGCGCTCGGAGGCTCGTGGA 1140	GCCCTCCTTCCTACTCA	당 왕
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1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGGGCCTCCTGCACCTCGAGGGTGAAGGCACTGTT 2041 CAGCGTGCTCAACTACGAGGAGAAGGCGCCCGGGCCTCCTGGGCGCCTCTGTGCTGGG	CCACCCATCCGTGGGCCGCCA 960	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCCCCCCCCC	pb 99
1921 CTTCATCCCCAAGCCTGACGGCCTGCGGCCGATCTGTGAACATGAGCTGACGTGGGGAGCT1921 CTTCATCCCCCAAGCCTGAAGAAAAAGAGGGCCGAGTCTCACCTCGAGGGTGAAGGCACTGTT	TGCCAGACCGCCGAAGAAGC 900	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGAG 	B 8
1861 GGAAGCAGAGGTCAGGCAGGCATGGGGAAGCCAGGCCCGCCC	CTGGGCCACCCGGCAGGAC 840	781 TGCCCTIGAGCCGGAGCGGACGCCGTTGGGCAGGGTCCTGGGCCACCCGGCCAGACAGA	8 8
1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCAGACTGCAGACTGCGAAGCAGCAGCAGGCAG		21 GAGGC	Db :
1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	CCTGCCAGCCCGGGTGCGAG 720 CAAGAGGCCCAGGCGTGGCGC 780	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGG 721 GAGGCGCGGGGGCAGTTGCCAGCCGAAGTCTGCCGTTGCC	& B
1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	CGAG 7	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGGTCCCCCCTGGGCCCTGCCCAGGCCCCGGGTG	Ş
	C 660	601 TCAGGCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGG	P 6
1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCT	O	41 GGCTC	B *
1621 GAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAAGATCCTGGC	CTGCGCGCTCTTTGTGCTGGT 540 GTACCAGCTCGGCGCTGCCAC 600	481 CCGCGIGGGCCAACGACGIGCIGGTICACCIGCIGGCACGCIGCIGCCCICTITIGIGCIGCI 541 GCCTCCIAGCTTACGCCTACCAGGTGTGCGGCGCTGTTACCAGCTCGCCGCTGCCAC	문

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CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCC
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                                                                                                         GAGTGTCCAGCACCCCGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA
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APPLICATION NUMBER: 08/912,951
APPLICATION NUMBER: 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1996
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-CCT-1996
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION: TO SEQUENCE CHARACTERISTICS:
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FILING DATE: 11-Jan-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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STATE: California
COUNTRY: United States of America
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LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
THERAPEUTIC METHODS
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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INAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hTRT"

/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches
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GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC
                             TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCCGGGCAGGAC
                                                                                                                                               GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC
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		OY 1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCGATGCC 60	Query Match 100.0%; Score 4015; DB 15; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-044-539-1	man telome: ase (hTRT)	; NAME/KEY: CDS ; LOCATION: 563454 ; OTHER INFORMATION: /product= "hTRT"	۰.	leic acid	; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 4015 base pairs		REFERENCE/DOCKET NUMBER: 015389-002600US TELECOMMUNICATION INFORMATION:	; ATTORNEY_AGENT INFORMATION: ; NAME: Apple, Kandolph T. ; REGISTRATION_UMBER: 36.429	7.	; APPLICATION NUMBER: US 08/844,419 ; FILING DATE: 18-APR-1997		-199 -199		; APPLICATION NUMBER: US/10/044,539 ; FILING DATE: 11-Jan-2002 ; CLASSIFICATION: 435 . DDTOP ADELICATION DATA.	; SOFTWARE: PatentIn Release #1.0, Version #1.30; CURRENT APPLICATION DATA:	; MEDIUM TYPE: FLORDY GISK ; COMPUTER: IBM PC COMPATIBLE ; OPERATING SYSTEM: PC-DOS	FORM:	RY: U		NUMBER OF SEQUENCES: 335		Chapman, Karen B. Morin, Gregg B. Harlev, Calvin
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3121 TCACCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTGTGACAGGCCTC	Qy Db Qy	2041 CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCTGGGCGCCTCTGTGCTGGG 2100
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2821 GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCCGGACCCTGGAGGT	Qy Db	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1
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341 CGTCTC	S B &	1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCGGGGGGGG
		1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

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RESULT 12
US-10-325-810-1
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                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: CURROWN>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             Nakāmura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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STATE: California
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   APPLICATION NUMBER: US/09/402,181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4015; Conserv
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: AUSENTHAR 42,271
REGISTRATION NUMBER: 015189-002620US
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OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
                                                                                                                                                     GGACCCGGCGCTTTCCCGCGCGCGCTGGTGCCCAGTGCCTGGTGTGCCTTGGGACGC
                                                        CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC
                                                                                                                                 NAME/KEY:
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Pred. No. 0;
0; Mismatches
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                                        CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCCAGCCAAGGGCT
                                                                                ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA
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Sequence 1, Application US/10388578

Publication No. US20030224411A1

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: John, Brandenberger
APPLICANT: John, Irving
APPLICANT: Mok, Michael
APPLICANT: Mok, Michael
APPLICANT: Mok, Michael
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Dow
TITLE OF INVENTION: Embryonic Stem Cells
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Custom
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
COTHER INFORMATION:
US-10-388-578-1
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US-10-388-578-1
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Sequence 1, Application US/10449565

Publication No. US20030225027A1

GENERAL INFORMATION:
APPLICANT: Huang, Jun Jian
APPLICANT: Huang, Cui-Fen
APPLICANT: Huang, Cui-Fen
APPLICANT: King, Hsiang-fu
TITLE OF INVENTION: Telomerase Reverse Transcriptase Fragments and Uses thereof
FILE REFERENCE: 9661-037

CURRENT APPLICATION NUMBER: US/10/449,565

CURRENT APPLICATION NUMBER: 0/384,806
PRIOR APPLICATION NUMBER: 60/384,806
PRIOR FILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 4015

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2702)..(3454)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches
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61 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	QY Db		ु र
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1321 AGCCGGTGTCTGTGCCCGGAGAAGCCCCAGGGTTGTGGCGGCCCCCAAGAGAGAAGAAGAAGAAGAAGAAGAAGAA		1 ACGGCCGCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCCTG	ਲੇ ਵ
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Sequence 1. Application US/10602441

Publication No. US20040106128A1

GENERAL INFORMATION:
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APPLICANT: Forlkis, Maria
APPLICANT: Forlkis, Maria
APPLICANT: Forlkis, Maria
APPLICANT: Wang, Zhuo
IITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Revei
FILE OF INVENTION ITANScriptase
FILE REFERENCE: 086/002
CURRENT APPLICATION NUMBER: US/10/602,441
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/393,295
PRIOR APPLICATION NUMBER: 60/393,295
PRIOR TILING DATE: 2002-06-27
INUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                            ; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
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  Query Match 100
Best Local Similarity 100
Matches 4015; Conservative
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3900	AGGTGGAGACCCTGAGAAGGACCCTGGGAACTTTGGAGTGACCAAAGGTGTG	3841	뫄
3900		3841	V
3840	CCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTTCCTT	3781	₽
3840		3781	Ą
3780	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCCACATAGGAATAGTCCATCC	3721	DЬ
3780	GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3721	Ą
3720	GAGTGTCCAGCACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3661	DЬ
3720	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3661	V
3660		3601	рb
3660	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAAGCCAAGGGCT	3601	Ş
3600	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAG	3541	Дb
3600	CACACCCAGGCCCGCACCGCTGGGGAGTCTGAGGCCTGAGTGAG	3541	Ş
3540	GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGG	3481	Вb
3540	GAGCAGACACCAGCAGCCCTGTCACGCCCGGGCTCTACGTCCCAGGGAAGGGAGGG	3481	Ş
3480	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCCCCCACAGCCAGGCCGA	3421	뮍
3480	. ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA	3421	γŞ
3420	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC	3361	Дb
3420	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGGCCGCAGCCCAACCCGGC	3361	γQ
3360		3301	Db

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